Sequence

Sequence 11, Appl Sequence 2, Appli Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 33, Appl Sequence 11, Appl Sequence 12, Appli Sequence 13, Appli

US-08-346-455B-11 US-08-977-221-11 PCT-US95-06613-11 PCT-US95-11684-4 US-08-701-582D-13 US-09-063-893A-19 US-09-042-785A-23

ALIGNMENTS

US-08-652-877-86
US-07-822-043-11
US-08-479-722B-2
US-08-479-722B-3
US-08-37-682-043-33
US-08-37-221-33
US-08-977-221-33
US-08-977-221-33
US-108-977-221-33

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Sequence 69, Application US/08346455B

Fatent No. 5731LT7

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.

APPLICANT: UNITED STATES OF AMERICA; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK
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CITY:
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COUNTY:
COUNTY:
U.S.A.
ZIP: 10154
ZONDUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER:
COMPUTER:
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COMPUTER:
COMPOTING SYSTEM:
COMPOTING SYSTEM:
COMPOTING SYSTEM:
CONTROLING DATA:
APPLICATION NUMBER:
CLASSIFICATION DATA:
APPLICATION NUMBER:
PRING APPLICATION DATA:
PRING DATE: 28 NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE: 24 NAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 20749.182
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION INFORMATION:
TELECOMMUTICATION INFORMATION:
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TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69.
SEQUENCE CHARACTERISTICS:
4655
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TOPOLOGY: Unknown
MOLECULE TYPE: CDNA
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(without alignments)
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/fB_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/fB_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTrS_COMB.pep:*
                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-346-4558-67

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US-08-346-4558-38

US-08-977-221-38

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US-09-112-450-4
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US-09-014-969-19
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                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                 RESULT 2
US-08-977-221-69
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                                                                                                                                                                                                                                                                                     121 SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAAECPAGFVRPPLIIFSVDGFRASYMK 180
                                                                                                                                                                                                                                                                                                                                          KGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRVAPKRRQERPVAPPKKRRR 360
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                                                                                                                                                                                                                                                                                                               121 SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180
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                                                                                                                     Length 915;
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                                                                                                                       DB 1;
                                                                                                                                                 0; Mismatches
                                                                                                                       Score 5019;
Pred. No. 0;
                          NAME/KEY: A2058 ATX protein
                                                                                                                       100.0%;
100.0%;
                                                                                                                                                   Matches 915; Conservative
                                                   DENTIFICATION METHOD:
COTHER INFORMATION:
US-08-346-455B-69
                                                                                                                                      Local Similarity
 HYPOTHETICAL:
FEATURE:
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                                                                                                                       Query Match
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                                                                   APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
Sequence 69, Application US/08977221
Patent No. 6084069
GENERAL INFORMATION:
                                                                                                                                                                                                                                 MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEO ID NO: 69
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    : 345 PARK AVENUE NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 915; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-977-221-69
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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345 PARK AVENUE

NEW YORK U.S.A.

NEW YORK

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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/29,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/ACENT INFORMATION:
NAME: DOROTHY R AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 36,434
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFAX: (212) 751-6849
                                                                                                      SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
                                                                   MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEÓ ID NO:
SEQUENCE CHARACTERISTICS:
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; OTHER INFORMATION:
PCT-US95-06613-69
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                        COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                            ZIP: 10154
            CITY: NEW STATE: NI COUNTRY:
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NAME/KEY: A2058 ATX protein

TOPOLOGY: Unknown

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Length 915;
                Indels
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DB
100.0%; Score 5019;
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
Query Match
Best Local Similarity
Matches 915; Conserv
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APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUIZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
WUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:

MORGAN & FINNEGAN

ADDRESSEE:

Sequence 69, Application PC/TUS9506613 GENERAL INFORMATION:

RESULT 3 PCT-US95-06613-69

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ARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMC 566
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                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: Unki
                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
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                                                                                                                                                                                                                                                                                           STRAIN:
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              RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQH 480
                                                                  LPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDHGFUNKVNSMQTVF 540
                                                                                                                                                                 VGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTNTFRPTMPEEV 600
                                                                                                                                                                                                                       TRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTEERHLLYGRPAVLYRT 660
                                                                                                                                                                                                                                                                            RYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCL 720
                                                                                                                                                                                                                                                                                                                                   AYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASER 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/08346455B
Patent No. 5731167
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA, DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 28-NOV-199
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OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
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                                     NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 758-4800
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: SEQUENCE CHARATERISTICS:
LENGTH: 829
TYPE: amin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 4533; DB Pred. No. 0; 0; Mismatches
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.3%;
Best Local Similarity 99.9%;
Matches 828; Conservative
                                                                                                                                                                                                                                                                            SSS: single
Unknown
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE: Melanoma
CELL LINE: A2058
                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Human
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421 ARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMC 480
                       TVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKY
                                                                                                                                                                             DAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPIFDYDYDGLHDTEDKIK
                                                                                                                                                                                                                                 QYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESK
                                                                         PKNKLDELNKRLHTKGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSY
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
STREET: AS PARK AVENUE
                                                                                                                                                                                                                                                                                  WVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESEI 915
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REFERENCE/POCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSTEM: PC-DOS/MS-DOS
WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 34, Application US/08977221
; Patent No. 6084069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Floppy Disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
: U.S.A.
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STATE: NEW YORK
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US-08-977-221-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 90.3
Best Local Similarity 99.9
Matches 828; Conservative
                                                                                                                                                                                                                                                                                                                                     LOCATION:
IDENTIFICATION METHOD:
                                 TOPOLOGY: Unknown MOLECULE TYPE: protein HYPOTHETICAL: NO
                single
                                                                                                                                                                                                                                     CELL TYPE: Melanoma CELL LINE: A2058
                                                                                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
    STRANDEDNESS: SING
amino acid
                                                                                                               ORGANISM: Human
                                                                                            ORIGINAL SOURCE:
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COTHER INFORMATION: Putative protein
COTHER INFORMATION: sequence of A2058 Autotaxin
PCT-US95-06613-34
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                                                                                                                          Score 4533;
Pred. No. 0;
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US-08-346-455B-67
; Sequence 67, Application US/08346455B
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Best Local Similarity
                           LOCATION
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ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
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ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NEW YORK
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              GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 861;
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89.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
                                                                                                            STRET: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: U C. ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: N-tera 2D1 ATX protein
                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DOROTHY R. AUTH
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: Unknown
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COTHER INFORMATION:
US-08-346-455B-67
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                                                        DHER----PSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPV 352
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                                                                                                                                          353 APPKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDH
                                                                                                                                                                                                                          413 GMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQH
                                                                                                                                                                                                                                                                                                          FKPYLKQHLPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDHGFDNK
                                                                                                                                                                                                                                                                                                                                                                                          53 VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTNTF
                                                                                                                                                                                                                                                                                                                                                                                                             593 RPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTEERHLLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 67, Application US/08977221
Patent No. 6084069
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                297 DHERLRSMPSILSNL----ISLDTNMPFGPE--
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OF DAYS

SOFTWARE: WOLDSELL.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06613

-- THG DATE: 24-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy Disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LS: ADDRESS:
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FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        893 KTSRSYPEILTLKTYLHTYESEI 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 34
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GRCFELQEAGPPDCRCDNLCXSYTSCCHDFDELCLXTARAWECTKDRCGEVRNEENACHC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
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89.1%; Pred. No. 0;
ive 12; Mismatches
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                                                                                  APPLICATION NUMBER: US/08/977,221
                                                                                                                                       CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/29,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DOROTHY R. AUTH
REGIETRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 758-4800
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: N-tera 2D1 ATX
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TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
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US-08-977-221-67
                                                            CURRENT APPLICATION
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Best Local Similarity
                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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538
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                                                                                          RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVS 712
                                                                                                                                                                                     PSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVL 772
                                                                                                                                                                                                                                                                               VKKYASERNGVNVISGPIFDYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQ 832
                                                                                                                                                                                                                                                                                                                                                                                                                                       833 PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFR 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
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PADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFR 892
                                                     VKKYASERNGVNVISGPIFDYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQ
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 08/249,182
FILING DATE: 15-MAY-1994
PRIOR APPLICATION NUMBER: 07/82,043
FILING DATE: 17-JAN-1993
ATTONNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DOROTHY R. AUTH
REGISTRATION UNBER: 36,434
REFERENCE,DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/08346455B; Sequence 38, Application US/08346455B; Patent No. 5731167; GENERAL INFORMATION:
                                                                                                                                                                                                893 KTSRSYPEILTLKTYLHTYESEI 915
                                                                                                                                                                                                                  KTSRSYPEILTLKTYLHTYESEI 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 38
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTEERHLLYG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 653 RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVS 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713 PSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVL 772
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHERLRSMPSILSNL----ISLDTNMPFGPE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 GMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKPYLKQHLPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDHGFDNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTNTF
                                                                                                                                                                                                                                                                                                                                                                                                70;
                                                                                                                                                                                                                                                                                                                                                            Length 861;
                                                                                                                                                                                                                                                                                                                                                                                              19; Indels
                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                           ; Score 4418; DE; Pred. No. 0; 12; Mismatches
REFERENCE/DOCKET NUMBER: 2026-4149US2
                                                                                                                                                                                                                                   NAME/KEY: N-tera 2D1 ATX protein
           TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           88.0%;
89.1%;
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.1%
Matches 822; Conservative
                                                                                                                                        SIMANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                   CT-US95-06613-67
                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                         861
                                                                                                                                                                                                                                                 LOCATION
                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                    61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARAWECTKDRCGEVRNEENACHC 120
                                                                                                                                                                                                                                                                                                                                                                                                                  121 SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGF--RASY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                     MKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 EDVICD -- RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQH 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 MDGRCHMYRTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKALIANLTCKKPDQH 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600 DRPAVLYRTRYDILYHTDFESGYSEIFLMPLWTSYTVSKQAEVSSVPBHLTSCVRPDVRV 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVI----PHERRILTILRWLT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 LPDHERPSVYAFYSEOPDFSGHKHMPFGPE------324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 PKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGM 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKPYLKQHLPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDHGFDNK 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   653 -RPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLJTSCVRPDVRV 711
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                                                                                                                                                                                                                                                   70;
                                                                                                                                                                                                                 DB 1; Length 979;
                                                                                                                                                                                                                Ouery Match 85.3%; Score 4279; DB 1; Length 9
Best Local Similarity 87.1%; Pred. No. 0;
Matches 805; Conservative 13; Mismatches 36; Indels
                                                                                                                                 OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
                                                                                                 LOCATION: IDENTIFICATION METHOD:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                   US-08-346-455B-38
                                                                                 NAME/KEY:
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QPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFF
                                                                                                                                                                                                                                                                                                   APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/977,221 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                        915
                                                                                                                                   863
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; Sequence 38, Application US/08977221
; Patent No. 6084069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                        RKTSRSYPEILTLKTYLHTYESEI
                                                                                                              840 RKTSRSYPEILTLKTYLHTYESEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 38
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein uvportHFTICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE
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CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NEW YORK COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW YORK
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IDENTIFICATION METHOD:

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APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: PROTELLY STIMULATING
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: putative autotaxin
CTHER INFORMATION: protein sequence from PCT-US95-06613-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENT CONTROL TO THE TOTAL THE T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                     Sequence 38, Application PC/TUS9506613 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.3%;
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IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW YORK
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE:
CELL TYPE:
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ORGANELLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                       121 SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGF--RASY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 EDVTCD--RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKALIANLTCKKPDQH 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVI----PHERRILTILRWLT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 LPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 PKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGM 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKPYLKQHLPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFOGDHGFDNK 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                          1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 MKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVF
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                                                                                                                                             Query Match 85.3%; Score 4279; DB 3; Length 979; Best Local Similarity 87.1%; Pred. No. 0; Matches 805; Conservative 13; Mismatches 36; Indels 70;
OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
US-08-977-221-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     892 RKTSRSYPEILTLKTYLHTYESEI 915
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APPLICANT: UNITED STATES OF AMERICA; DEPT.
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: N-tera 2D1 putative OTHER INFORMATION: ATX protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 2026-4149PCT TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800 TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 28 NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WORDFELL.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE: teratocarcinoma CELL LINE: N-tera 2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DOROTHY R. AUTH
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
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727; Conserv
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                                                                                                                                                                                                                                                                                                                  ZIP: 10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 VNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTNTF 592
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                                                                                                                                                                                                                           61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
                                                                                                                                                                                                                                                                                                     121 SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGF--RASY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 PKKRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGM 414
                                                                                                                                                                       MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVI----PHERRILTILRWLT
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                                                                                                                 Indels
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                                                                                              87.1%; Pred. No. 0;
tive 13; Mismatches
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Matches 805; Conserv
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CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHCSEDCLARGDCCTNYO 135
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Length
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 DB 1;
76.5%; Score 3842; D
85.6%; Pred. No. 0;
Live 12; Mismatches
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ZIP: 10154
COMPUTER READABLE FORM:
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                                                                                                                           FILING DATE:
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                                                     SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKFNHR 253
                                                                                                            WWGGQPLWITATKQGVKAGTFFWSVVI----PHERRILTILRWLTLPDHERPSVYAFYSE 309
                                                                                                                                                                  QPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAPPKKRRKIHRMDHYA 369
                                                                                                                                                                                                                        370 AETRODKMTNPLREIDKIVGOLMDGLKOLKLRRCVNVIFVGDHGMEDVTCD--RTEFLSN 427
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| Sequence 36, Application US/08977221
| Patent No. 6084069
| GENERAL INFORMATION:
| APPLICANT: UNITED STATES OF AMERICA; DEPT.
| APPLICANT: OF HEALTH AND HUMAN SERVICES
| TITLE OF INVENTION: MOTILITY STIMULATING
| TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
| TITLE OF INVENTION: THERAPY
| NUMBER OF SEQUENCES: 69
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MORGAN & FINNEGAN
| STREET: 345 PARK AVENUE
| CITY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70; Gaps
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                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/49,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRANTON NUMBER: 2026-41490S3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: N-tera 2D1 putative CTHER INFORMATION: ATX protein sequence US-08-977-221-36
                                                              SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
                                              PC-DOS/MS-DOS
MEDIUM TYPE: Floppy Disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE: teratocarcinoma CELL LINE: N-tera 2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLOGUEST 188
LENGTH: 788
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
IDENTIFICATION METHOD:
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                                          OPERATING SYSTEM:
SOFTWARE: WordPer
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                                                                 370 AETRODKMINPLREIDKIVGOLMDGLKQLKLRRCVNVIFVGDHGMEDVTCD--RTEFLSN 427
                                                                                    250 ------MPNPLREMHKIVGQLMDGLKQLKLHRCVNVIFV---ETMDGRCHMYRTEFLSN 299
                                                                                                                                                      488 ANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTF 547
                                                                                                                                                                                                                                                                                            608 IMYLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTEERHLLYG-RPAVLYRTRYDILY 666
                                                                                                                                                                                                                                                                                                                                                                 HTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCLAYKNDK 726
                                                                                                                                                                                                                                                                                                                                                                                                                                  QMSYGFLFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASFRNGVNVI 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGPIFDYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSF 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      847 ILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKT 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 KYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPG 607
                                                                                                                                    428 YLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: STREEKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFWANN, ELLIOTT; KRUIZSCH,
APPLICANT: HENRY; MURATA, JUN
APPLICANT: HENRY; MORATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF SEQUENCES: 69
CORRESPONDENCES: 69
                 235 QPDFSGHKHMPFGPE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36, Application PC/TUS9506613 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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780 YLHTYESEI 788
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119 SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKFNHR 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 VVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGF--RASYMKKGSKVMPNIEKLR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WWGGQPLWITATKQGVKAGTFFWSVVI----PHERRILTILRWLTLPDHERPSVYAFYSE 309
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Best Local Similarity 85.6%; Pred. No. 0;
Matches 727; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: N.tera 2D1 putative (OTHER INFORMATION: ATX protein sequence PCT-US95-06613-36
                                                                                                                                        APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 QPDFSGHKHMPFGPE------
                    08/346,455
                                                                               08/249,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE: teratocarcinoma CELL LINE: N-tera 2D1
                                                                                                                                                                                                                                                                                TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346
FILING DATE: 26-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
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419
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300 YLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHY 359
              547
                                       607
            HTDFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCLAYKNDK
                                                                                                                                             SGPIFDYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSF
                                                                                                                                                                     ILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKT
                                      KYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPG
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Search completed: July 23, 2001, 13:22:17 Job time: 370 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

July 19, 2001, 14:43:22; Search time 25.97 Seconds Run on:

(without alignments)
2683.855 Million cell updates/sec

US-09-483-831-69 5019

Perfect score:

1 MARRSSFQSCQIISLFTFAV......RSYPEILTLKTYLHTYESEI 915 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

**76174552** residues 219241 seqs, Searched:

hits satisfying chosen parameters: ō Total number

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

PIR 68:\* Database

pir1:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	autotaxin precurso	plasma cell membra	cell surface antiq		plasma cell membra	nucleotide pyropho	nucleotide pyropho	nucleotide pyropho	hypothetical prote		probable phophodie	hypothetical prote	phosphodiesterase-	hypothetical prote	protein kinase PC-	hypothetical prote				w		hypothetical prote	-	hypothetical prote	tyrosine protein k	hypothetical prote	latent transformin	glucocorticoid-sen	protein-tyrosine k
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	DB	<u>.</u> –	٦	-	-	П	7	7	7	~	7	~	~	~	7	7	7	~	7	~	~	7	~	Н	7	~	7	7	~	7
	Length	915	882	875	925	905	457	496	479	829	461	485	429	433	674	300	743	493	614	133	96	453	360	329	465	1186	462	1820	454	1374
оP	Query Match	100.0	85.8	41.5	39.0	37.8	12.9	12.2	12.2	12.2	12.1	10.7	10.4	9.5	9.1			6.7		4.8	4.7	٠	٠	2.9	2.9	٠	5.6		•	2.4
	Score	5019	4306	2084	1955.5	1899.5	646.5	612	611.5	610	609	539.5	522	461	456.5	456	410	335.5	297.5	241.5	238	238	163	146.5		142	132	127	•	122
,	Result No.	-	7	۳	4	Z.	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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probable histidine	hypothetical prote	66K glycoprotein p	tenascin precursor	nuclease NUC1 (EC	hypothetical prote	sulfite reductase	transforming growt	hypothetical prote	position-specific	fibrillin 1 precur	fibrillin I - bovi	hypothetical prote	hypothetical prote	vitronectin precur	probable membrane
02	<u> </u>	01	22	88		27	56	99	17	17	57	4,	37		15
T0382	T3900	A3834	JQ132	T11588	S6971	S6134	A3562	T2056	A2963	A4722	A5556	T1867	T2878	SGMS	S6719
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2471	1888	475	2019	335	686	1035	1394	2911	1394	3002	2871	3147	753	476	1472
2.4	2.4	2.4	2.4	2.3	2.3	2.5	2.5	2.3	2.2	2.2	2.5	2.2	2.2	2.5	2.2
121.5	121	119.5	119	117	116.5	112	112	112	111	111	110.5	110.5	110	109.5	109.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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Autoctaxin precursor - human

Altoctaxin precursor - human

Altoctaxin precursor - human

Nicontrains: phosphodisesterase I (EC 3.1.4.1)

C.Species: Homo saplens (man)

C.Accession: A55144; A4229

R.Murata, J.; Lee, H.Y.; Clair, T.; Krutzsch, H.C.; Arestad, A.A.; Sobel, M.E.; Liott

J. Balol. Chem. 269, 34979-3484, 1994

A.Accession: A55144; MUID:95074054

A.Accession: A55144; MUID:95074054

A.Accession: A55144; MUID:95074055; PIDN:AAA64785.1; PID:9537906

A.Accession: A55144; MUID:95074055; PIDN:AAA64785.1; PID:9537906

A.Accession: A55144; MUID:95074054

A.Accession: A55144

A.Accession: A5145; MUID:92129337

A.Accession: A4329

A.Accession: A44504-507, AAV;510, X,511-515;533-548;S,7554-559, NV,561-

A.Eccesion: A4329

A.Accession: A4329

A.Accession: A4329

A.Accession: A4329

A.Accession: A4329

A.Accession: A44504-507, AAV;510, X,511-515;533-548;S,7554-559, NV,561-

A.Accession: A44504-507, AA
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Gaps ; DB 1; Length 915; Indels .; 0 100.0%; Score 5019; 100.0%; Pred. No. 0; tive 0; Mismatches Ouery Match 100.0 Best Local Similarity 100.0 Matches 915; Conservative

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1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60 ð

1 MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60 g 61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120 61 g ò

SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180 121 ò

pred

9;

Gaps 9 59

94; 885;

120

173 170 233

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nucleotide diphosphohydrolase
A; Beference number: JU0187
A; Reference number: JU0187
A; Reference number: JU0187
A; Recession: JU0187
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-66, 'Q', 68-81, 'T', 83-94, 'C', 96, 'A', 98-195, 'A', 197-514, 'E', 516-621, 'E'
A; Experimental source: strain Sprague-Dawley
C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C; Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric dies
F; 54-97/Domain: somatomedin B homology <SBH1>
F; 98-141/Domain: somatomedin B homology <SBH2>
F; 53,150,396,408,522,608,829/Binding site: carbohydrate (Asn) (covalent) #status F; 207/Binding site: AMP (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK
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|MARQGCLGSFQVISLFTFAISVNICLGFTASRIKRAE-WDEGPPTVLSDSPWTNTSGSCK
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plasma cell membrane glycoprotein PC-1, brain specific - rat
N'contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 5.5pecies: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A55453; JU0187
R;Narita, M.: Goli, J.: Nakamura, H.; Sano, K.
J. Biol. Chem. 269, 28235-28242, 1994
A;Title: Molecular cloning, expression, and localization of a brain-specific;
A;Recession: A55453; MUD:95050605
A;Accession: A55453
A;Molecule type: mRNA
A;Residues: 1-885 <NAR>
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A; Residues: 1-885 <NAR>
A; Cross-references: GB:D28560; NID:g464196; PIDN:BAA05910.1; PID:g464197
R; Narita, M.; Goli, J.; Sano, K.; Nakamura, H.
submitted to JIPID, February 1994
       TFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTILRWLTLPDHER
                                                                                                                                                                                                PSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAPPKKRRR
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Page 3

QY 513 VYKKPSGKCFFQGDHGFDNKVNSMQTVFYGXGPTFKYKTKVPPFENIELYNVMCDLLGLK 572	588 648 748 708 808 768 828	RESULT 4 A39216 A30216 C302199 A20216 C302199 A20216 A30216	A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-925 ABUC> A; Cross-references: GB:J05654 A; Cross-references: GB:J05654 A; Cross-references: GB:J05654 A; Frunakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S A; Frunakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S A; Title: Molecular cloning of CDNAs for human fibroblast nucleotide pyrophosphatase. A; Reference number: S21706 A; Reference number: S21706 A; Status: not compared with conceptual translation A; Molecule type: mRNA A; Residues: 1-925 <funi>A; Residues: 116-121; 247-271, 'X', 273-275; 279-280, 'X', 282-283; 303-316; 362-364; 449-465; 4</funi></funi></funi></funi></funi></funi>	A; Note: it is uncertain whether Met-1 or Met-53 is the initiator R;Belli, S. I.; Goding, J.W. Eur. J. Blochem. 226, 433-443, 1994 A;Title: Blochem. 226, 433-443, 1994 A;Title: Blochem. 226, 43030 A;Reference number: S51030; MUID:95094801 A;Accession: S51030 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-80 <bel> C;Genetics: A;Gene: GDB:PDNP1; M6S1; NPPS A;Cross-references: GDB:132615; OMIM:173335 A;Cross-references: GDB:132615; OMIM:173335 C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology C;Keywords: coenzyme A; glycoprotein; phosphoricin; phosphoric diester hydrolase; t F;77-97/Domain: transmembrane #status predicted <twm> F;77-97/Domain: transmembrane</twm></bel>
QY         809 VEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSFILPHRPDNEESCNSSEDESKWV 868           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 3 A57080 cell surface antigen RB13-6 - rat N; Contains: phosphodiesteras I (EC 3.1.4.1) C; Species: Rattus norvegicus (Norway rat) C; Species: Rattus norvegicus (Norway rat) C; Species: Rattus norvegicus (Norway rat) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Accession: A77080 C; Accession: A77080 C; Accession: A77080 A; Title: Affinity purification and cDNA cloning of rat neural differentiation and tumor A; Reference number: A57080; MUID: 95247775 A; Accession: A77080 A; Status: preliminary A; Accession: A77080 A; Residues: 1-875 cDDI: A; Cross-references: GB: Z47987; NID: 9806378; PIDN: CAA88029.1; PID: 9806379 C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology C; Reywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase; sur F; 1-22/Domain: cytosolic #status predicted ccyty	F;23-45/Domain: transmembrane #status predicted <tmm> F;46-875/Domain: extracellular #status predicted <ext> F;46-875/Domain: somatomedin B homology <sbh2> F;51-94/Domain: somatomedin B homology <sbh2> F;51-94/Domain: somatomedin B homology <sbh2> F;206/Binding site: AMP (Thr) (covalent) #status predicted F;237,280,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status pr Query Match  Query Match  41.5%; Score 2084; DB 1; Length 875; Best Local Similarity 43.5%; Pred. No. 5e-135; Matches 386; Conservative 160; Mismatches 248; Indels 94; Gaps 11;</sbh2></sbh2></sbh2></ext></tmm>	Qy         57 GSCKGRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEEN 116           11:::::::::::::::::::::::::::::::::::	QY         279 VIPHERRILTILRWLTLDDHERPSVYAFYSEQPDFSGHKXGPFGPEESSYGSPFTPAKRP 338           1:1   1:1:1   1   1   1   1   1   1   1

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F;104-144/Domain: somatomedin B homology <SBH1>
F;145-188/Domain: somatomedin B homology <SBH2>
F;179,285,341,477,578,585,643,700,731,748/Binding site: carbohydrate (Asn) (covalent)
F;256/Binding site: AMP (Thr) (covalent) #status predicted
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LHRCLNLILISDHGMEQGSCKRYIYLNKYLGDVKNIKVIYGPAARLRPSDVPDKYYS--- 468
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RESULT A27410

A; Accession: 159055
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: 159055
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 203-219 < RES>
A; Cross-references: GB:M12552; NID:g200234; PIDN:AAA39892.1; PID:g200235
A; Cross-references: GB:M12552; NID:g200234; PIDN:AAA39892.1; PID:g200235
A; Title: Identification and characterization of a soluble form of the plasma cell mem
A; Reference number: S38354; MUID:94039066
A; Accession: S38354
A; Molecule type: DNA
A; Molec mem predict cDNA and anal <u>ဗ</u> н from 16; plasma cell membrane glycoprotein PC-1 - mouse
N;Alternate names: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 05-May-2000
C;Accession: A27410; I59055; S38354
R;van Driel, I.R.; Goding, J.W.
J; Biol. Chem. 262, 4882-4887, 1987
A;Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from A;Reference number: A27410; MUID:87165906
A;Accession: A27410. 265 399 | :||:|| ||||| :| :|| || || : LDKCLNLILISDHGMEQGSCKKYVYLNKYLGDVNNVKVYGPAARLRPTDVPETYYSFNY 453 237 280 IPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPK 339 457 A; Molecule type: mRNA A; Residues: 1-905 <VANA A; Cross-references: GB:J02700; NID:g200236; PIDN:AAA39893.1; PID:g200237 A; Note: the authors translated the codon CAG for residue 24 as Glu R; Van Driel, I.R.; Wilks, A.F.; Pietersz, G.A.; Goding, J.W. R; Van Liel, A.G. Sci. U.S.A. 82, 8619-8623, 1985 A; Title: Murine plasma cell membrane antigen PC-1: Molecular cloning of CA, Reference number: IS9055; MUID:86094275 -----VIKALQKVDRLVGMLMDGLKDLG SCKGRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENA CHCSEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRAS YMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPV RKVAPKRRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLK LRRCVNVIFVGDHGMEDVTCDRTEFLSNYLINVDDITLVPGTLGRIRSKFSNNAKY--DP 37.8%; Score 1899.5; DB 1; Length 905; 41.0%; Pred. No. 2.4e-122; Indels 262; 238 FDATFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFW-365; Conservative 155; Mismatches 400 394 ò

Oy 364 RWDHYAAETRODKHTNPLREIDKIVGQLANGIKGLKIRRCVNVIFVGDHGMEDVTCDRTE 423  231	Score 612; DB 2; Length 496;
158 154 154 158 158 158 158 158 158 158 158 158 158	RESULT 6 T09932 UUCleotide pyrophosphatase homolog T16L4.200 - Arabidopsis thaliana CiSpecies Arabidopsis thaliana (mouse-ear cress) CiDate: 16-JU1-1999 #sequence_revision 16-JU1-1999 #text_change 15-Oct-1999 CiScession: 10932 Ribevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, June 1999 Accession: 709932 Accession: 70932 Accession: 70932 Acce

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A;Gene: CESP:C27A7.1
A;Map position: 5
A;Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;
                                                                                         Query Match
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Matches
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A; Cross-references: EMBL:281041; PIDN:CAB02784.1; GSPDB:GN00023; CESP:C27A7.1
A; Experimental source: clone C27A7
C; Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19494
B;Harris, B
submitted to the EMBL Data Library, October 1996
A;Reference number: 219132
                                                     C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: T03293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 VFLDELAPWIKLEEDWVLSMTPLLA--IRPPDDMSL-PDVVAKMNEGLGSGK-----V 362
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A.Reference number: 214889
A.Accession: T03293
A.Accession: T03293
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-479 <HSI>A.Cross references: EMBL:U25430; NID:9818848; PID:9818849
A.Experimental source: strain Tainung 67
C.Genetics:
A.Note: OSE4
                                                                                       C;Accession: T03293
R;Hsing, Y.C.; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
submitted to the EMBL Data Library, April 1995
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A;Molecule type: DNA
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                                     nucleotide pyrophosphatase homolog - rice
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Best Local Similarity
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A; Status: preliminar
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nucleotide pyrophosphatase homolog T16L4.210 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999 C;Accession: T09933 R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTV
          Length 829;
12.2%; Score 610; DB 2; 23.9%; Pred. No. 6.5e-34;
                                                                                                                                                                                                            192; Conservative 127; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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----ILLDYTATIFDVERISGFQF 807
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A;Accession: T33724
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: LNB
A;Residues: 1-429 <LEE>
A;Cross-references: EMBL:AF086791; NID:93820581; PID:93089614; PIDN:AAC70363.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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R.Lee, J.S.; Jin, S.J.; Kang, H.L.; Kang, H.S.
submitted to the EMBL Data Library, August 1998
A.Description: Sequence analysis of 67E10 cosmid clone of Zymomonas mobilis: A.Reference number: 221392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Zymomonas mobilis
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                        HGIVGNSMYDPVFDATFHLRGREKFNH--RWWG-GQPLWITATKQGVKAGTFFW--SVVI 280
                                                                                                                                      385 DKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNY--LTNVDDITLVPGTL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 DIVIGELIEGLKKRRIDKHVNIIFLSDHGMAPTSDNRLIWLDNMFNLSAVAHRDAWP--L 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 GGFRGESDLDDEXIXESLVNYSRSSLPSAENWNVYSKKDIPSRWHYSNNERIAPVWMIPD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 RRWHVAR------KPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFK-YK 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 LVKIDQTIGQLVQGLKQRGIK--ANLVIVSDHGMAATSSDRVVALNKILDPSLYHVVTGG 290
                                                                                                                                                                                                               ----TILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPE 324
                                                                                                                                                                                                                                                                                                                  35 ESSYGSPFTPAKRPKKVAPKRRQERPVAPPKKRRKIHRMDHYAAETRQDKMTNPLREI 384
                                                                                                                                                                                                                                                                                                                                                                     ----- 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 GRIRSKFSNNAKYDPKAIIANLTCKKPD-QHFKPYLKQHLPKRLHYANNRRIEDIHLLVE 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 VGWSLVSMLDHSPELEYEPL------GVHGYDNLSPVMRALFIASGSSFKNFK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VNDN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 LREIDKIVGQLADGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPG 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 RPPLIIFSVDGFRASYMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 SEADIEGVRPEMWRQFDSHVPFSERVDQVFSWLAYPKKKRPQFITLYFENVDHAGHLYGP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92; Gaps
  166 LIIFSVDGFRASYMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPES
                             PESHCIVGNSMYDPVFDATFHLR---GREKFNHRWWG-GQPLWITATKQGVKAGTFFW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SVVIPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.4%; Score 522; DB 2; Length 42
Best Local Similarity 29.2%; Pred. No. 3e-28;
Matches 127; Conservative 63; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 GKKLAPFQNTEIYGILSHILDLPAQPNNGTYEGALP--LRRN 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 -TKVPPFENIELYNVMCDLLGLKPAPNNGTH-GSLNHLLRTN 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein - Zymomonas mobilis
                                                                                                                                                                                                               281 PHERRIL----
                                                                                                        226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T40657
R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, November 1998
A; Reference number: 221889
A; Reference number: 221889
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 1-485 < LXIN>
A; Status: 1-485 < LXIN>
A; Cross references: EMBL: AL034352; PIDN: CAA22177.1; GSPDB:GN00067; SPDB: SPBC725.05c
A; Experimental source: strain 972h-; cosmid c725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 WIQAYSPVLAINPQWGKDVENQSEKNAEVVAKWNEALSSGKVKNGEFLKVYLKEKLPERL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:::|| |:|| |:| | 357 HFSESYRIPPIIGIVGEGLMVRQN-----RTNAQVCY--GDHGYDNELFSMRTIFVGHGS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPESHGIVGNSMYDPVFDATFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFW---- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 LKSSWTCPEGYCPHFNLSVPLEERVDSVLSHFDHLEDEVPDLLMLYFDEPDQSGHNYGPD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----- RVTTAV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 REIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGT 441
                                                                                                                                                                                                                                                                                                                                                                                                                      163 RPPLIIFSVDGFRASYMKKGSKVMPNIEKLRSCGTHSPY-MRPVYPTKTFPNLYTLATGL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPEESSYGSPFTPAKRPKRVAPKRRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPL 381
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SVVIPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------LGR-IRSKFSNNAKYDPKAIIANLTCK-KPDQHFKPYLKQHLPKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGP
                                                                                                                                                                                                                                                                                                               12.1%; Score 609; DB 2; Length 461; 31.9%; Pred. No. 3.5e-34; Live 78; Mismatches 127; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
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                                        A.Molecule type: DNA
A.Residues: 1-461 <BEV>
A.Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.210
A.Experimental source: cultivar Columbia; BAC clone T16L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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submitted to the Protein Sequence Database, June 1999 A; Reference number: 216897 A; Accession: T09933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 DP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 TFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGT 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 RFSRGKKVPSFENVQIYNVVAELLGLRPAPNNGS 443
                                                                                                                                                                                                                                                                                                                  Query Match 12.1%
Best Local Similarity 31.9%
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.7
Best Local Similarity 29.2
Matches 135; Conservative
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                                                                                                                                                                                                      A; Gene: ATSP:T16L4.210
A; Map position: 4
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Map position: 5
Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588/1
                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C27A7.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T19495
R; Harris, B.
submitted to the EMBL Data Library, October 1996
A; Accession: T19495
A; Accession: T19495
A; Accession: T19495
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: C27A7
A; CCOSs-references: EMBL: 281041; PIDN: CAB02785.1; GSPDB: GN00023; CESP: C27A7.3
A; Experimental source: clone C27A7
C; Genetics:
A; Gene: CESP: C27A7.3
A; Map position: 5
A; Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588,
                                                                                                                                                   | : |: || : || : || || 327 IVCQMHEGWNALSAAQITKRHPLQM-------GGSSGFDFMLPSMRAIFLANGPSFM 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESHWVDDDCEEIKAAECPA-GFVRPPLIIFSVDGFRASYMKKGSKVMPNIEKLRSCGTHS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYKWA--GCENL--GKCQIDGFSTPPLVILSFDGFAKEYLER--RIVKSLELIAECGVKA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 PYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDP-VFDATFHLRGREKFNHRWWGGQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAPPKKRRKIHRMDHYAAETR 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 ODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 IDTVNQELEEVNNYIDILMKALHDENLLECVNLVIVSDHGMQAL---NNSIEVETIVNMD 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 DITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRI 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 PLPGHESKVEAMLLGAHATYD------C-----WRKQALPTRWHYGTHPRIPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRVYPSFPSKTFPNHYTWVTGLYPESHGITDNYVFDPNLYPELLAMRKHEA - - KEFYQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNVTVPSFQNVQYMNLWLYLLGLEGTVDNNGTIGFFDSILKNPPIRENKWDSMEECLNFG
437 LVPGTLGRIRSK-FSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIED
                                                                                                                    496 IHLLVERRWH-----VARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLWITATKO--GVKAGTFFWSVVIPHERRILTILRWLTLPDHERPSVYAFYS---EQPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VGCYYNITGYMPD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 YKTKVPPFENIELYNVMCDLLGLK-PAPNNGTHGSLNHLLRTNTFRPTMPEEVTR-PNYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 674;
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                                                                                                                                                                                                                                      549 YKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTN 590
                                                                                                                                                                                                                                                                       377 PNLLLNPINNVDVYPLLTRLLGIAMAPNDGNPRALLQALRSS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
9.1%; Score 456.5; DB 2;
Best Local Similarity 23.8%; Pred. No. 1.7e-23;
Matches 170; Conservative 104; Mismatches 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Bringson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carraro, E.; Docena, C.; El-Dorry, H.; Fraincanil, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Muramee, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E. F.G.; Murame, E.C.; Myayati, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.B. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.J. and Silva, R.C.; Allonieri, D.B. M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A.Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphodiesterase-nucleotide pyrophosphatase precursor XF2599 [imported] - Xylella fasti
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sedner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004067; GB:AE003849; NID:99107818; PIDN:AAF85396.1; GSPDB:GN007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: B82537
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
A; Title: The genence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717
A; Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                291 AYAGIEPSSGHSLK-DLEPLFAS-----HDHMQCWPKQQIPARFHYGQNPRVPAVVCAA 343
                                                                                                                                                ERRWHVARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIE 560
                                                                                                                                                                              344 EVGWSIMGD--DSMAAHATK----GNHGYDNQTPEMGALFIANGPAFQKHKVIESMDNID 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 LIIFSVDGFRASYMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPES 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGIVGNSMYDPVFDATFHLRGREKFNH-RWWGGQPLWITATKQGVKAGTFFW----SVV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEES 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYGSPFTPAKRPKRVAPKRRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPLREIDK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----DIT 436
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                              441 TLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.2%; Score 461; DB 2; Length 433;
27.1%; Pred. No. 4.6e-24;
tive 65; Mismatches 152; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 IVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVD---
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Matches 125; Conservative
                                                                                                                                                                                                                                                                 561 LYNVMCDLLGLKPAP 575
                                                                                                                                                                                                                                                                                                                           VQPLVAQVLKLK-AP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Contents: annotation
C, Genetics:
A, Gene: XF2599
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35;

v 665 LYHTDFESGYSEIFLMIJWTSYTVSKOAEVSSVPDHITSCYRPDVRVSPSESON 718	QY 452 NAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLLVERRWHVARRPL 511
.   :	Db 142 IAKSDRIERLTFYLDPQWQLALNPS 166
	QY 512 DVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGL 571 : :
756	QY 572 KPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKNKL 631                     Db 221 TPAPNNGTH
27	632 DELNKRLHTKGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTVSKQ
ESULT 15 41179	Db 230 239
n kinase PC-1 (EC 2.7.1) - bovine (fragments) rnate names: MAFP; major acidic fibroblast growth factor-s les: Bos primigenius taurus (cattle)	QY 692 AEVSSVPDHLTSCVRPDVRVSPSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKY-DAFL 750  1   1   1   1   1   1   1   1   1   1
;Uare: Z6-May-1992 #Sequence_revision ZZ-Apr-1995 #text_cnange 30-Apr-1999 ;Accession: A41179; A49308 Zdod, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S. Riol Chem 266, 16791-16795 1991	Qy 751 VTNMVPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPIFDYDYDGLHDTEDKIKQYVE 810
Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein kit Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein kit Teference number: A41179; MUID:91358477	234 IINIVERINGSEUVI. 811 GSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKWVEE
;Molecule type: protein ;Residues: 1-26;36-56;59-67;68-133;134-144;145-267;268-300 <oda>&gt;</oda>	Db 268HESLWVEE 275
Ē	Qy 871 LMKMHTARVRDIEHLTSLDFFRK 893  : :    :  :    :      276 LLKLHTARITDVEHITGLSFYQQ 298
	000
.Molecule type: protein .Molecule type: protein .Residues: 27-35,'X',37-58 < 002>	Search completed: July 19, 2001, 14:40:54 Job time: 152 sec
<pre>;Experimental source: liver ;Note: sequence extracted from NCBI backbone (NCBIP:141583) ;Note: sequence extracted from NCBI backbone (NCBIP:141583) ;Note: sequence extracted pyrophosphatase; somatomedin B homology ;Keywords: glycoprotein; phosphoprotein; phosphotransferase ;1-25/Domain: somatomedin B homology (fragment) <sbh> ;36/Binding site: AMP (Thr) (covalent) #status predicted</sbh></pre>	
Query Match 9.1%; Score 456; DB 2; Length 300; Best Local Similarity 18.7%; Pred. No. 6.3e-24; Matches 150; Conservative 45; Mismatches 86; Indels 522; Gaps 14;	
y 107 RCGEVRNEENACHCSEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPL 166	
y 167 IIFSVDGFRASYMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESH 226 	
Y 227 GIVGNSMYDPVFDATFHLRGREKFNHRWWGGQPLWITATKGGVKAGTFFW 276	
y 277SVVIPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSP 331   :	
y 332 FTPAKRPKRKVAPKRRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQL 391	
0 109 108	
y 392 MDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSKFSN 451	

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 19, 2001, 14:44:18 ; Search time 16.91 Seconds (without alignments) 1853.564 Million cell updates/sec

US-09-483-831-69 5019 1 MARRSSFQSCQIISLFTFAV.....RSYPEILTLKTYLHTYESEI 915

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 93435 seqs, 34255486 residues Searched:

93435

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		mus m	P25353 saccharomyc	P39997 saccharomyc	P15396 bos taurus	P08466 saccharomyc	P98164 homo sapien	-	-	P81203 cunninghame	P22458 oryctolagus	Q10480 schizosacch	P32898 saccharomyc	P22064 homo sapien		drosc	рошо	OO8600 mus musculu	P29788 mus musculu	P98133 bos taurus	001975 caenorhabdi				P40798 drosophila		P11205 newcastle d	Q61554 mus musculu				homo	P22105 homo sapien
SUMMAKIES	DI	PC1_HUMAN	PC1_MOUSE	YCR6_YEAST	YEB6_YEAST	PPD1_BOVIN	NUC1_YEAST	LRP2_HUMAN	LT23_CAEEL	YDT2_SCHPO	NUC1_CUNEE	VTNC_RABIT	NUC1_SCHPO	YD30_YEAST	TGFB_HUMAN	NUCG_BOVIN	ITA2_DROME	FBN1_HUMAN	NUCG_MOUSE	VTNC_MOUSE	FBN1_BOVIN	YJ05_CAEEL	ATC9_YEAST	NUC1_SYNRA	YDZ2_SCHPO	STC_DROME	YNI7_YEAST	RRPL_NDVB	FBN1_MOUSE	POLG_PEMVM	MTDM_PARLI	TENA_CHICK	TENA_HUMAN	TENX_HUMAN
	DB	-	Н	П	П	П	П	7	П	Н	П	П	П	-	٦	Ч	Н	-	-	7	-	٦	-	-	-	-	-	<b>-</b>	-	-	-		Н,	-
	Query Match Length	873	871	743	493	61	329	4655	1323	1888	252	475	335	686	1394	299	1396	2871	294	478	2871	753	1472	320	1065	1106	1178	2204	2871	3099	1612	1808	2201	4289
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BFR1_YEAST AMIA_STRPN	DPOM_NEUIN NUCG_HUMAN	PIOU_HSV/J BAR3_CHITE PP11_HUMAN	EGER_DROME IDS_MOUSE FNBA_STAAU
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## ALIGNMENTS

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(See http://www.isb-sib.ch/announce/
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EXTRACELLULAR (POTENTIAL).
SOMATOMEDIN-B LIKE.
SOMATOMEDIN-B LIKE.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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1 24 CYTOPLASMIC (POTENTIAL).
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modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                      EMBL; M57736; AAA63237.1; --
EMBL; D12485; BAA02055.1; --
EMBL; D12485; BAA02053.1; ALT_INIT.
EMBL; AF067177; AAD38420.1; --
EMBL; AF067178; AAD38421.1; --
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InterPro; IPR002591; -
Pfam; PF01663; Phosphodiest; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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P06802;
01-JAN-1988 (Rel. 06, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-AUZ-2000 (Rel. 39 Last annotation update)
PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1 [INCLUDES: ALKALINE
PHOSPHODIESTERASE (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE
(EC 3.6.1) (NPPASE)].
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MEDLINE=91271356; PubMed=1647027;
Rebbe N.F., Tong B.D., Finley E.M., Hickman S.;
"Identification of nucleotide pyrophosphatase/alkaline phosphodiesterase I activity associated with the mouse differentiation antigen PC-1.";
Proc. Natl. Acad. Sci. U.S.A. 88:5192-5196(1991).
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J. Biol. Chem. 262:4882-4887(1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
          -!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
-!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 -----VIKALOKVDRLVGMLMDGLKDLG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCKGRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 SCKGRCFERIFS---NCRCDAACVSLGNCCLDFQETCVEPTHIWTCNKFRCGEKRLSRFV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 CHCSEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRAS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 CSCADDCKTHNDCCINYSSVCQDKKSWVEETCESIDTPECPAEFESPPTLLFSLDGFRAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 YMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPV 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 MNASFSLKSKEKFNPLWYKGQPIWVTANHQEVKSGTYFWPGSDVEIDGILPDIYKVYNGS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 IPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 RKVAPKRRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLK 399
                                                                                                                                                                                                                                                                                                                                                                                                                       Duplication; Signal-anchor; Hydrolase. BLOCKED.
                                                                 -:- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O - 2 MONONUCLEOTIDE.
-:- SUBUNT: HOWDIMER, DISULFIDE-LINKED.
-:- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
-:- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF ANTIBODY-SECRETING CELLS.
-:- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.8%; Score 1899.5; DB 1; Length 871; llarity 41.0%; Pred. No. 1.7e-129; Conservative 155; Mismatches 262; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 VPFEERILAVLEWLQLPSHERPHFYTLYLEEDDSSGHSHGPVSSE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80848F81071F70AA CRC64;
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Sci. U.S.A. 82:8619-8623(1985)
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                                                                                                                                                                                                                                                                             EMBL; J02700; AAA39893.1; ALT_INIT.
EMBL; M12552; AAA39892.1; -.
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PROSITE; PS00524; SOMATOMEDIN_B;
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Pfam; PF01033; Somatomedin_B; 2.
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MOD_RES ?1 ?1
DOMAIN 1 24
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MGD; MGI:97370; Pdnpl.
InterPro; IPR001212; -.
InterPro; IPR002591; -.
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871
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                                                     OLIGO-NUCLEOTIDES.
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les 365; Conserv
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CARBOHYD
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CARBOHYD
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     688 VSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKY- 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 FLRNDQFSR--DDFSNCMYQDLRIPLSPVHKCSYYKSNSKLSYGFLTPPRLNRVSNHIYS 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            761 QNSRVIRSQEILIPTHFFIVLTSCKQLSETPLECSA-LESSAYILPHRPDNIESCTHGKR 819
400 LRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKY--DP 457
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                                             518 SGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNN
                                                                                                                                                                                                                                                                                                                                GTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIM - - - YLQSDFDLGCTCDDKVEPKNKLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 LNKRLHTKGSTEERHLL----YGRPAVLYRTRY-DILYHTDFESGYSEIFLMLLWTSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747 DAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPIFDYDYDGLHDTEDKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q---YVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSED
                                                                                                                                                KAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKP
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  820 ESSWVEELLTLHRARVTDVELITGLSFYQDRQESVSELLRLKTHLPIFSQE 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 84.9 KDA PROFEIN IN PMP1-FENZ INTERGENIC REGION
YCRO26C OR YCR26C OR YCR246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           864 ESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESE 914
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Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
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Yeast 8:205-213(1992).
-i- SIMILARITY: TO YEAST YEL016C.
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Best_Local Similarity 24.8
Matches 116; Conservative
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                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPD1_BOVIN
P15396;
                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                    Query Match
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PPD1_BOVIN
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                                                                                                                                                                                                        164 PPLIIFSVDGFRASYM-KKGSKVMPNIEKLRSCG----THSPYMRPVYPTKTFPNLYTLA 218
                                                                                                                                                                                                                    TGLYPESHGIVGNSMYDPVFDATFHLRGREKFNHRWWGG---QPLWITATKQ----GVK 270
                                                                                                                                                                                                                                                                           285 AATHWWPGSDVNYTKYKTEEKLQPEHKKPIARERTPFYFDEFNAKEPLSGKLSKIIEYVD 344
                                                                                                                                                                                                                                                                                                                                                                                                                        354 PPKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                378 -----YY-----EDFTETLGEVDTFLKQLVESLQERNLTSFTNLVIVSDHG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 MEDVTCD-------RTEFLSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 MSDIVVPSNVIIWEDLLDEKLRKDYVSH-----AYLEGPMMAISLKDSGNI----NE 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 IIANLTCKKPDQHFKPYLKQHLPKRLHY--ANNRRIEDIHLLVERRWHVARKPL----- 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 VYHNLKTSIDEDKYTVYVNGNFPKEWNFNDGKNHHMASIWIVPEPGYAVMKKEQLKKVAK 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 -DVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLG 570
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                                                                                                                                                                                                                                                                                                                                                                    LPD-HERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRVAPKRRQERPVA 353
                                                                                                                                                  Ouery Match 8.2%; Score 410; DB 1; Length 743;
Best Local Similarity 24.0%; Pred. No. 5.4e-22;
Matches 126; Conservative 76; Mismatches 178; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288C / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 35, Last annotation update)
HYPOTHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571 LKPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFD 616
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                                                                                               POTENTIAL.
EMBL, X59720; CAA42318.1; -.
PIR; S19437; S19437.
PIR; S273800; S27380.
SGD; S0000621; YCR026C.
InterPro; IPR002591; -.
Ffam; PF01663; Phosphodiest; 1.
Hypothetical protein; Transmembrane.
TRANSMEM 114 135 POTENTIAL
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                                                                                                                                                                                                                                                                                                                271 AGTFFW-----
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P39997;
                                                                                                            SEQUENCE
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YEB6_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLRDKRLQKLIGEVDGFFLDLIEGLQKRNLLKISNVMIVSDHGMSNVNANDGEHVVVWER 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 YPIEHGIVSNIFWDNFTSSEFR---PNNLDARIWSNTADPIWQLLQTESQGEYKVATHMW 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SVV-----IPHER------RILTILRWLTLPD-HERPSVYAFYSEQ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LSNYLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQ---HFKP 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 VFPADAMSAFISHLYN----EGPMMWYCLKNPRDKQWICDLIEAQLEKAYGDEISRKFHV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            476 YLKQHLP---KRLHYANNR-----RIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDH 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 IIFSVDGFRASYM-KKGSKVMPNIEKLRSCG----THSPYMRPVYPTKTFPNLYTLATGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 YPESHGIVGNSMYDPVFDATFHLRGREKFNHRWWG--GQPLW--ITATKQG-VKAGTFFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 PDFSGHKYGPFGPEESSYGSPFTPAKŔPKRKVAPKRRQERPVAPPKKRRKIHRMDHYAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 VDSYGHSFG-----Y
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1-APR-1990 (Rel. 14, Last sequence update)
01-FBE-1994 (Rel. 28, Last annotation update)
PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 127;
   Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 493;
Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570
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24.8%; Pred. No. 7.6e-17;
ative 71; Mismatches 153;
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InterPro; IPR002591; -
Pfam; PF01663; Phosphodiest; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHODIESTERASE) (FRAGMENT).
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al protein.
493 AA; 57354 MW;
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Inner membrane.
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SEQUENCE
                                                                                                                                                                                                                                         EMBL;
PIR; S
PIR; S
HSSP;
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                                                                                J. Biol. Chem. 260:8320-8324(1985).
-!- CATALYIT CACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
SUCCESSIVELY FROM THE 3-'HYDROXY TERMINI OF 3-'HYDROXY-TERMINATED
OLIGO-NUCLEOTIDES.
                                                                                                                                                                                                                                                                172 DGFRASYMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGN 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vincent R.D., Hofmann T.J., Zassenhaus H.P.;
"Sequence and expression of NUC1, the gene encoding the mitochondrial
nuclease in Saccharomyces cerevisiae.";
Nucleic Acids Res. 16:3297-3312(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purnelle B., Coster F., Goffeau A.; "The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies 24 open reading frames including NUC1, PRP21 (SPP91), CDC6, CRZ2, the gene for S24, a homologue to the aconitase gene ACOI and two homologues to chromosome III genes."; Yeast 10:1235-1249(1994).
                                  Culp J.S., Blytt H.J., Hermodson M., Butler L.G.;
"Amino acid sequence of the active site peptide of bovine intestinal
5'-nucleotide phosphodiesterase and identification of the active
site residue as threonine.";
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                              Overproduction of yeast viruslike particles by strains deficient in a mitochondrial nuclease.";
                                                                                                                                                                   FORMS A PHOSPHOTHREONINE INTERMEDIATE. 580C8B4807A61C84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of yeast chromosome X.";
Yeast 10:1657-1662(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                               Score 238; DB 1; Length 61;
Pred. No. 5.4e-11;
9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRIAL NUCLEASE (EC 3.1.30.-).
NUC1 OR YJL208C OR J0310 OR HRE329.
                                                                                                                                                                                                                                                                                                                                                   PRT;
           TISSUE=Intestine;
MEDLINE-85234541; PubMed-2989287;
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MEDLINE-90014786; PubMed-2552292;
Liu Y., Dieckmann C.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88233924; PubMed=2836792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95242842; PubMed=7725802;
                                                                                                                                                                                                                4.78;
                                                                                                                                                                              61 AA; 6999 MW;
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                               PIR; A25274; A25274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1988
                                                                                                                                          Hydrolase.
                                                                                                                                                                                                                                                                                                                                                  NUC1_YEAST
P08466;
                                                                                                                                                                  ACT_SITE
SEQUENCE
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Best Local S
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P98164; 000711; 016215;
01-0CT-1996 (Rel. 34, Casted)
15-DEC-1998 (Rel. 37, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
1COW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
(GLYCOPROTEIN 330).
LRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 LEHITPESLAARNADRKNSFFKEDEVIPEKFRGKLRDYFR-SGYDRGHQAPAADAKFSQQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 685 SYTVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCLAYKNDKQMSYGFLFPPY-LSSSPE 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       744 AKYDAFLVTNMVPMY-PAFKR-VW---NYFQRVLVKKYASERNGVNVISGPIFDYDYDGL 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  565 MCDLLGLKPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDK 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 VEPKNKLDELNKRLHTKGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWT 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 --PTQKPNS-NIQSHSFNVDPSGFFKYGFPGPI----HDLQNREEFISCYNRQTQNPYWV 91
MOI. Cell. Biol. 9:3323-3331(1989).
-!- FUNCTION: THIS ENZYME HAS BOTH RNASE AND DNASE ACTIVITY.
-!- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM.
-!- SUBGUIT: HOMODIMER.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           799 HDTEDKIKQYVEGS--SIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRP-DNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01223; Endonuclease; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
Hydrolase; Nuclease; Endonuclease; Magnesium; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  856 ESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEIL 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAEC9678CB00943C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.9%; Score 146.5; DB 1;
22.8%; Pred. No. 0.002;
Ive 48; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X06670; CAA29870.1; -.
EMBL; X77688; CAA54748.1; -.
EMBL; Z34098; CAA84003.1; -.
EMBL; Z49483; CAA84003.1; -.
EMBL; M28067; AAA34457.1; -.
PIR; S05888; NOBYN1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 22.8%;
Matches 79; Conservative
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P13717; 1SMN.
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PROTEIN 2
                                                                                                                                               Pfam; PF00008; EGF; 13.
Pfam; PF00058; 1dl_recept_a; 36.
Pfam; PF00058; 1dl_recept_b; 37.
PRINTS; PR00261; LDLRECEPTOR.
           U33837; AAB41649.1;
U04441; AAB02882.1;
S73145; AAB30825.1;
                                                                          InterPro; IPR00003; -. InterPro; IPR000152; -. InterPro; IPR000561; -.
                                                                                                                       InterPro; IPR001881; -. InterPro; IPR002172; -.
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695
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                                                                   600073;
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                          EMBL;
EMBL;
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                                                     HSSE;
 Kounnas M.Z., Loukinova E.B., Stefansson S., Harmony J.A.K.,

Rewer B.H., Strickland D.K., Argraves W.S.;

"Identification of glycoprotein 330 as an endocytic receptor for

"apolipoprotein J/Clusterin.";

J. Biol. Chem. 270:13070-13075(1995).

"I. FUNCTION: BINDS SPECIFICALLY CLUSTERIN WITH HIGH AFFINITY, BUT

ALSO LIGANDS IN COMPONENTS, PLASMINOGEN ACTIVATOR PLASMINOGEN

EXTRACELLUIAR MATRIX COMPONENTS, PLASMINOGEN ACTIVATOR INHIBITOR TYPE I COMPLEX, ADOLIPOPROTEIN E-PRRICHED

BETA-VLDL, LIPOPROTEIN LIPASE, LACTOFERRIN AND CALCIUM.

C. I- FUNCTION: RECEPTOR-MEDIATED UPTAKE OF POLYBASIC DRUGS SUCH AS

APROTIUM, AMINGINCASIDES AND POLYMENTS BE SIMILARITY).

PARA-THYROID-HORMONE-RELATED PROTEIN RELEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                        Hjaelm G., Murray E., Crumley G., Harazim W., Lundgren S., Onyango I., Ek B., Larsson M., Juhlin C., Hellman P., Davis H., Aekerstroem G., Rask L., Morse B., "Cloning and sequencing of human gp330, a Ca(2+)-binding receptor with potential intracellular signaling properties.";

Eur. J. Blochem. 239:132-137(1996).
                                                                                                                                                                                                                                                                                                MEDLINE-95048397; PubMed-7959795;
Korenberg J.R., Argraves K.M., Chen X.N., Tran H.,
Strickland D.R., Argraves W.S.;
"Chromosomal localization of human genes for the LDL receptor family member glycoprotein 330 (LRP2) and its associated protein RAP
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 4139-4406 FROM N.A.
MEDLINE=94244704; PubMed=8187828;
Lundgren S., Hjaelm G., Hellman P., Ek B., Juhlin C., Rastad J.,
Klareskog L., Aakerstrom G., Rask L.;
A protein involved in calcium sensing of the human parathyroid and
placental cytotrophoblast cells belongs to the LDL-receptor protein
superfamily.";
Homo sapiens (Human).
Vertebrata; Euteleostomi;
Vertebrata; Euteleostomi;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-ASSOCIATED PROTEIN (RAP).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: ABSORPTIVE EPITHELIA, INCLUDING RENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROXIMAL TUBULES.
-!- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.
-!- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
-!- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 4 SH3-BINDING DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAIN.
                                                                                                                                                                                                                                 Knaak C., Argraves W.S.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                TISSUE=Kidney;
MEDLINE=96305376; PubMed=8706697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95286588; PubMed=7768901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3xp. Cell Res. 212:344-350(1994).
                                                                                                                                                                                                                                                                          SEQUENCE OF 3833-4453 FROM N.A.
                                                                                                                                                                                                       SEQUENCE OF 2705-4453 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              Genomics 22:88-93(1994).
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                     rissue=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION
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LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
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EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
PROSITE; PROUDLY LUDARACETION.
PROSITE; PROUDLY EGF_1: 1.
PROSITE; PSO0022; EGF_1: 1.
PROSITE; PSO1186; EGF_2: 9.
PROSITE; PSO1187; EGF_2: 9.
PROSITE; PSO1187; EGF_2: 3.
PROSITE; PSO1068; LDLRA_1: 31.
PROSITE; PSO6068; LDLRA_2: 36.
Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane; Receptor; EGF-1ike domain; Signal; POlymorphism.
SIGNAL
                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDL-RECEPTOR CLASS B 10.
LDL-RECEPTOR CLASS B 11.
LDL-RECEPTOR CLASS B 12.
LDL-RECEPTOR CLASS B 13.
LDL-RECEPTOR CLASS B 14.
EGF-LIKE 7.
                                                                                                                                                                                                                                                                                                                          LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 7.
EGF-LIKE 1.
                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
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LDL RECEPTOR CLASS A 9 .
LDL RECEPTOR CLASS A 10 .
LDL RECEPTOR CLASS A 11 .
LDL RECEPTOR CLASS A 11 .
LDL RECEPTOR CLASS A 12 .
LDL RECEPTOR CLASS A 14 .
LDL RECEPTOR CLASS A 14 .
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EGF-LIKE 4.
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EGF-LIKE B.
LDL-RECEPTOR CLASS B
LDL-RECEPTOR CLASS B
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Db 1456 HINTSLUENGSYLVANDEDSISGRIFWSDATQGKTWSAPQRGTDRRWYFDSILITETIA 1515  Cy 246GREEF	RESULT 8 LT23_CAEEL  ID LT23_CAEEL  AC P24348; DT 01-MAR-1992 (Rel. 21, Created) DT 01-MAR-1992 (Rel. 21, Last sequence update) DT 01-MAR-1992 (Rel. 21, Last sequence update) DT 01-OCT-2000 (Rel. 40, Last sequence update) DT 01-OCT-2000 (Rel. 40, Last sequence update) DE LET-23 RECEPPOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112). GN LET-23 RECEPOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112). GN LET-23 RECEPOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112). GN LET-23 RELOGATION-TYROSINE KINASE PRECURSOR (EC 2.7.1.112). GN LET-23 RELOGATION-TYROSINE KINASE PRECURSOR (EC 2.7.1.112). GN LET-23 RELOGATION-TYROSINE KINASE PRECURSOR (EC 2.7.1.112). GN NOBI_TAXID-6239; RN [1] RP SEQUENCE FROM N.A. RX MEDININE-91089019; pubMed-1979659; RM Aroian R.V., Koga M., Mendel J.E., Ohshima Y., Sternberg P.W.; RA Aroian R.V., Koga M., Mendel J.E., Ohshima Y., Sternberg P.W.; RT "The let-23 gene necessary for Caenorhabditis elegans vulval
FT DOMAIN 2202 2244 LIDL-RECEPTOR CLASS B 23. FT DOMAIN 2296 2298 LIDL-RECEPTOR CLASS B 24. FT DOMAIN 2299 2313 LIDL-RECEPTOR CLASS B 24. FT DOMAIN 2290 2214 LIDL-RECEPTOR CLASS B 25. FT DOMAIN 2519 2517 LIDL-RECEPTOR CLASS B 25. FT DOMAIN 2519 2517 LIDL-RECEPTOR CLASS B 25. FT DOMAIN 2519 2517 LIDL-RECEPTOR CLASS B 26. FT DOMAIN 2519 2517 LIDL-RECEPTOR CLASS B 27. FT DOMAIN 2519 2777 LIDL-RECEPTOR CLASS B 27. FT DOMAIN 2519 2777 LIDL-RECEPTOR CLASS A 10. FT DOMAIN 2519 2777 LIDL-RECEPTOR CLASS A 11. FT DOMAIN 2519 2777 LIDL-RECEPTOR CLASS A 11. FT DOMAIN 2519 2777 LIDL-RECEPTOR CLASS A 12. FT DOMAIN 2519 2777 LIDL-RECEPTOR CLASS A 12. FT DOMAIN 2519 2777 LIDL-RECEPTOR CLASS A 23. FT DOMAIN 2510 2510 LIDL-RECEPTOR CLASS A 23. FT DOMAIN 3511 2510 LIDL-RECEPTOR CLASS A 23. FT DOMAIN 3512 2510 LIDL-RECEPTOR CLASS A 39. FT DOMAIN 3512 2510 LIDL-RECEPTOR CLASS A 39. FT DOMAIN 3512 3510 LIDL-RECEPTOR CLASS A 39. FT DOMAIN 3512 3510 LIDL-RECEPTOR CLASS A 39. FT DOMAIN 3513 3510 LIDL-RECEPTOR CLASS A 39. FT DOMAIN 3514 3515 LIDL-RECEPTOR CLASS A 39. FT DOMAIN 3516 2510 LIDL-RECEPTOR CLASS A 39. FT DOMAIN 3517 3521 LI	QY         69        AGPPDC

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CARBOHYD
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                                                                                                                                                                       induction encodes a tyrosine kinase of the EGF receptor subfamily."; Nature 348:693-699(1990).
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Pfam; PF00757; Furin.iike; 1.
Pfam; PF01030; Recep_L_domain; 2.
Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Transmembrane; Glycoprotein; Receptor; Signal.
                                                        Sakai T., Roga M., Ohshima Y.;
Genomic structure and 5' regulatory regions of the let-23 gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                     Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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ATP (BY SIMILARITY).
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                                       STRAIN=BRISTOL N2;
MEDLINE=96177760; PubMed=8604137;
                                                                                                                                                                 MEDLINE=94147981; Pubmed-8313880;
                                                                            the nematode C. elegans.";
J. Mol. Biol. 256:548-555(1996).
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                                                                                                                  STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | | :: | | :| | :| | 341 CSDGHHYDATKDVRECEKCRSSSCPK-----ICTVDGHLT-----NETLKNLEGCE 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 LSNYLTNVDDITLVPGTLGRIRSKFSNNA-KYDPKAIIAN-----LTCKKPDQHFKPY 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KILYNSDFGNRMECVH-----DCPVSHFPTQKNVCEKCHPTCYDNGCTGPDSN- 638
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Best Local Similarity 18.4%; Pred. No. 0.73;
Matches 149; Conservative 106; Mismatches 290; Indels 264; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        225 NDKCWGSGDNDCQRVYRSVCPKSCSQCFYSNSTSSYEC-CDSACLGGCTGHGPKNCIACS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 -HDFDELCLKTARGWECTKDRCGEV----RNEENACHCSEDC----LARGDCCTNYQVV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 CKGESHW--VDD--DCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIEKLR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 QIDGH----LIIEHAFTYEQLKVLETVKIVSEYITIVQQNFYDLKFLKNLQIIEGRKLHN 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 AFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAPPKKRRRKIHR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 LKQHLPKRLHYAN-NRRIEDIHLLVERRWHVARKPL--DVYKKPSGKCFFQGDHGFDNKV 533
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                                                                                                                                                                                                                                                                                                                                                                            ----KSYTSCC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 SCGTHSPYMRPVYPTKTFPNLYTLAT-GLYPESHGIVGNSMYDPVFDATFH-LRGREKFN
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(POTENTIAL).
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                                                                                                                                                                                                   6B0307EE53EEFA99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            48 SDSPWTNISGSCK------GRCFELQEAGPPDCRCDNLC--
                                           C -> Y (IN SY10).
-> R (IN MN216).
-> W (IN MN23).
-> Y (IN SY11).
-> F (IN SY16).
N-LINKED (GLCNAC.
                         GLCNAC.
                       N-LINKED
C -> Y (1)
G -> R (1)
C -> W (1)
C -> Y (1)
T -> J (1)
G -> F (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYG-----KKAPKFLRVFARSSSHIPKMIRRKRQMDSKKYFSFDKESDRQV--- 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --IDQVLSDWYSGKHELVQQ------S100VLSDWYSGKHELVQQ-----S10VLSDWYKKPSDSKSVGGN 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKR-------LHYANNR 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNNSFIKTOG-LNSILQLDIVTHPFKSVYAFSCLFNIQDDVFKTFEKLKDTFETVLENLP 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYGSPFTPAKRPKRKVAPK-----RRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GIMYLOSDF-DLGCTCDDKVEPKNKLDELNKR 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                         Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIEDIHLLVERRWHVARKPLDVY-----KKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I-----FSVNSKKHSVNINAKTAANNGLSHLQNFSEELLKKRKLFSSLFSNNVSYKKSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 2.4%; Score 121; DB 1; Length 1888; Local Similarity 17.2%; Pred. No. 1.4; nes 123; Conservative 101; Mismatches 223; Indels 26
                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 217.4 KDA PROTEIN C6B12.02C IN CHROMOSOME I.
SPAC6B12.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8AD3BBCE32397C29 CRC64;
                                                                                                                       Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNNG---THGSLNHLLR----TNTFRPTM------
    PRT; 1888 AA
                                                                                                         Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
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   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 886
935
997
1053
1356
1665
                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=4896,
                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
YDT2_SCHPO
014207;
                                                                                                                                                                                                             STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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638 LHTKGSTEERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLW-TSYTVSKQAEVSS 696
                                                                              697 VPDHLISCVRPDVRVSPSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKYDAFLVTNMVP 756
                                                                                                                   ---DITVIDIL-- 870
                                                                                                                                                          757 MYPAFKRVWNYFQRVLV----KKYA-----SERNGVNVIS------GPIF 791
                                                                                                                                                                                                 ----FLESWSILNHILFHVYKKKYALWEQVNSFFDLOKKELSILEMEKIWYVIMTLNPVF 926
                                                                                                                                                                                                                                        792 DYDYDG-------LHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKC 837
                                                                                                                                                                                                                                                                           927 QIGLNGTTHSPGNNSFWPLIIRVSESAFKMHKDGHNVKVVERYLRTVFLRIHFLISEWRW 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sednence of
                      -!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
                                                                                                                                                                                                                                                                                                                                                 838 DGPLSVSSFI---LPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HO H.-C., Liu F.-C., Chung J.-G., Chen L.-Y.;
"Purification, characterization and complete amino acid sequencese CI from Cunninghamella echinulata var. echinulata. Eur. J. Biochem. 256:112-118(1998).
-I- FUNCTION: THIS ENZYME HAS BOTH RNASE AND DNASE ACTIVITY.
-I- COFACTOR: REQUIRES MAGNESIUM OR MANGANESE FOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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ACT_SITE 87 87 BY SIMILARITY.
SEQUENCE 252 AA; 27498 MW; 2FA49B158AAABEC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
Cunninghamellaceae; Cunninghamella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 15-252 FROM N.A., AND SEQUENCE OF 1-49 STRAIN-ATCC 36190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.4%; Score 119.5; DB 1; Best Local Similarity 25.0%; Pred. No. 0.13; Matches 65; Conservative 33; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
(EC 3.1.30.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cunninghamella echinulata var. echinulata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98417435; PubMed=9746353;
                                                                                                        846 GQSGLLECYR-NLRIQAS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001604; -.
Pfam; PF01223; Endonuclease; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=76406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998
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15-DEC-1998
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646 ERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTS--YTVSKQAEVSSVP-DHLT 702

us-09-483-831-69.rsp

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753 753 C -> 1065 1065 T -> 1074 1074 G -> 1323 AA; 150510 MW;
746
776
368
469
700
753
1065
CARBOHYD
CARBOHYD
VARIANT
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                                                                                                                                                                       induction encodes a tyrosine kinase of the EGF receptor subfamily."; Nature 348:693-699(1990).
                                                       Sakai T., Koga M., Ohshima Y.;
"Genomic structure and 5, regulatory regions of the let-23 gene in
                                                                                                                            Thomas K.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X57767; CAA40919.1; ALT_SEG. EMBL; D63426; BAA09729.1; ALT_INIT. EMBL; 270038; CAA93882.1; -... PIR; S13422; S13422. HSSP; P11362; 1FGI. WOTMPEP; ZK1067.1; CE03840. InterPro; IPR000494; -... InterPro; IPR000719; -..
                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-96177760; Pubmed-8604137;
                                                                                                                                                                 MEDLINE=94147981; PubMed=8313880;
                                                                             the nematode C. elegans.";
J. Mol. Biol. 256:548-555(1996).
                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                        MUTANTS
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43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -HDFDELCLKTARGWECTKDRCGEV----RNEENACHCSEDC----LARGDCCTNYQVV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKGESHW--VDD--DCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIEKLR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 SCGTHSPYMRPVYPTKTFPNLYTLAT-GLYPESHGIVGNSMYDPVFDATFH-LRGREKFN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 HRWWGG------QPLWITATKQGVKAGTFFWSVVIPHERRILTILRWLTLPDHERPSVY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 AFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAPPKKRRRKIHR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424
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                                                                                                                                                                                                                                                                                                                                                                                                                            225 NDKCWGSGDNDCQRVYRSVCPKSCSQCFYSNSTSSYEC-CDSACLGGCTGHGPKNCIACS 283
                                                                                                                                                                                                                                                                         Query Match 2.4%; Score 122; DB 1; Length 1323;
Best Local Similarity 18.4%; Pred. No. 0.73;
Matches 149; Conservative 106; Mismatches 290; Indels 264; Gaps
                                                                                                                                                                                                                                                                                                                                                                           48 SDSPWTNISGSCK-----KSYTSCC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 QIDGH----LIIEHAFTYEQLKVLETVKIVSEYITIVQQNFYDLKFLKNLQIIEGRKLHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --YVSKIDWSS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 -DSKLCETEQ-----RVCDK-----RVCDK-----ROCKRGCWGKEPEDCLECKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 LSNYLTNVDDITLVPGTLGRIRSKFSNNA-KYDPKAIIAN-----LTCKKPDQHFKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 LKQHLPKRLHYAN-NRRIEDIHLLVERRWHVARKPL--DVYKKPSGKCFFQGDHGFDNKV
.) (POTENTIAL) .) (POTENTIAL)
                                                 C -> Y (IN SY10).

G -> R (IN MN216).

C -> W (IN MN213).

C -> Y (IN SY11).

T -> I (IN SY16).

G -> E (IN SY7).

W; 6B0307BE53EERA99 CRC64;
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
C -> Y (IN SY10).
G -> R (IN MN216).
C -> W (IN MN23).
C -> Y (IN SY11).
T -> I (IN SY11).
G -> E (IN SY1).
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SEQUENCE
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                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
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P32898; Q04068;
01-0CT-1993 (Rel. 27, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 112.2 KDA PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 NERGQWEVQYRVIGNPPNVAVPTHFFKVII-----AEKSGEPTSSPSVAAFVLPNKP 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfan; PF01223; Endonuclease; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
Hypothetical protein; Hydrolase; Nuclease; Endonuclease; Magnesium; Mitochondrion; Inner membrane.
                                                                              -!- COFACTOR: REQUIRES MANGANESE OR MAGNESIUM (BY SIMILARITY).
-!- SUBGNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES PAMILY.
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MEDLINE=94040759; PubMed=8224861;
Ellis E.M., Reid G.A.;
"The Saccharomyces cerevisiae MTS1 gene encodes a putative
RNA-binding protein involved in mitochondrial protein targeting.";
Gene 132:175-183(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                             -! - FUNCTION: THIS ENZYME HAS BOTH RNASE AND DNASE ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.3%; Score 117; DB 1; Length 335; Best Local Similarity 29.8%; Pred. No. 0.28; Matches 37; Conservative 23; Mismatches 42; Indels
  Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z73099; CAA97354.1; -. InterPro; IPR001604; -.
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                                                       SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 IFSVDGFRASYMKKGSKVMPNI-EKLRSCGT----HSPYMRPVYPTKTFPNLYTLATG- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LYPES------HGIVGNSMYDPVFDATFHLRGREKFNHRWWGGQPLWITAIKQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 GV-----ERRILTILRWLTLPDHERPS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 VYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVAPPKKRRKI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------LMDG-----LKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 FILKVIGNILAMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA--VNLLTVGIQGVSDIEI 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 DYTFFPFSTTNPQDFANLRGVYLDSTLNP-----LLKQEDFDQEGWRLEHKNITDPES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329;
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I; 6CAD2EE5A6080D9C CRC64;
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Best Local Similarity 18.5%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                  11 18 Y
989 AA; 112180 MW;
                                                                                                                                                                                                                                                              EMBL; X70951; CAA50290.1; -. EMBL; U33007; AAB64877.1; -. PIR; S31321; S31321. SGD; S0002838; XDR430C.
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CONFLICT 11 1
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REFLIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
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EGF-LIKE 15.
EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                        REPEAT B.
EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL)
REPEAT C.
                      CALCIUM-BINDING (POTENTIAL)
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      PEROUENCE FROM N.A., AND PARTIAL SEQUENCE.

REQUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUB—Fibroblast, and Platelet;

MEDLINE—90275601; Pubmed—2350783;

MEDLINE—90275601; Pubmed—2350783;

MINAZONO K., Claesson-Welsh L., Heldin C.-H.;

Toff-beta l binding protein: a component of the large latent complex of TGF-beta l with multiple repeat sequences.";

Cell 61:1051-1061(1990).

CELL 61:1051(1990).

CELL 61:1051-1061(1990).

CELL 61:1051(1990).

CELL 61:1051(1990).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth factor binding: Repeat; EGF-like domain; Hydroxylation; Signal; Glycoprotein; Alternative splicing.

SIGNAL 1 20 POTENTIAL.

CHAIN 21 1394 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1.
                                                              724 HSLLDNEETFOREVVDKLTELOKYIVDTNNMNF----FITSDSDVQAKTVESQISKFMER 779
                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
LATENT TRANSFORMING GROWITH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWITH FACTOR BETA BINDING PROTEIN 1) (TGF-BETA1-BP-
                          WNY-----FQRVLV-----KKYASERNGVNVISGPIFDYDYDGLHDT-EDKIKQYVE-
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                        PRT; 1394 AA
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Pfam; PF00683; TB; 4.
PROSITE; PS00010; ASX_HYDROXYL; 13.
PROSITE; PS01082; EGF_1; 2.
PROSITE; PS01187; EGF_2; 11.
PROSITE; PS01187; EGF_CA; 15.
                                                                                                                          780 LPHGSCLPNGPKTSDYPLIGS 800
                                                                                                    ---GSSIP--VPTHYYSIITS
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                                                                                                                                                                                                                                        STANDARD;
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HSSP; P35555; 1EMO.
MIM; 150390; -.
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P22064;
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                                                                                                                           Gaps
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Cote J., Ruiz-Carrillo A.;
"Primers for mitochondrial DNA replication generated by endonuclease
                                                                                                                                                  PTVLSDSPWTNISGS----C----KGRCFELQEAGPPD-CR---CDNLCKSYTSCC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moos M. Jr., Nguyen N.Y., Liu T.-Y.;
"Reproducible high yield sequencing of proteins electrophoretically separated and transferred to an inert support.";
J. Blol. Chem. 263:6005-6009(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                       798 QHRHLCAHGQCRNTEGSFQCVCDQGYRASGLGDHCEDINECLEDKSVCQRGDCINTAGSY
     (POTENTIAL)
 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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W. DFFCA81A40B2C7D1 CRC64;
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                                                                                                2.2%; Score 112; DB 1; Length 1394; 23.8%; Pred. No. 4.1; ative 17; Mismatches 48; Indels 9;
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01-0CT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G)
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                                                                                                                                                                                                                                                                                                                        858 DCTCP-DGFQLDDNKTCQDINECEHP 882
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MEDLINE-88198128; PubMed-3360771;
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MEDLINE-95175374; PubMed-7870594;
98 98
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1039 1039
1394 AA; 152791 M
                                                                                                                          Conservative
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                                                                                                             Similarity
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P38447;
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Best Local S
Matches 49
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         797 GLHDTEDKIKQYVE----GSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHR 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 -LPRTEADGKSYVKYQVIGKNHVAVPTHFFKVLI------LEAAGGQIELRSYVMPNA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Gaps
                                                                                                                                                                                                                             InterPro: IPR001604; -...
Pfam; PF01223; Endonuclease; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
Hydrolase; Nuclease; Endonuclease; Mitochondrion; Transit peptide;
            SUBCELLULAR LOCATION: MITOCHONDRIAL.
SIMILARITY: BELONGS TO THE DNA/RNA NON-SPECIFIC ENDONUCLEASES
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                   MITOCHONDRION
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Job time: 171 sec
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SUBUNIT: HOMODIMER.
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Q9su81 arabidopsis

094323 schizosacch Ognam9 homo sapien 088027 rattus norv 069013 zymomonas m 0996x5 homo sapien 099697 mus musculu 09u1a9 homo sapien 09h15 caenorhabdi 09h15 homo sapien 09h15 homo sapien 09h15 homo sapien 09tsb2 bos tautus 09su80 arabidopsis 02129 caenorhabdi 04555 homo sapien 04555 mus musculu 045199 mus musculu 045199 caenorhabdi 045195 caenorhabdi 045195 mus musculu 045199 mus musculu 045199 treptomyce 055767 chilo iride 095767 chilo iride 095767 chilo iride 095767 chilo iride

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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	Description	Q13827 homo sapien	Q13822 homo sapien	Q15117 homo sapien	Q9rle6 mus musculu	Q64610 rattus norv	Q63490 rattus norv	P97676 rattus norv	P97675 rattus norv	P70641 rattus norv	014638 homo sapien	Q9npz3 homo sapien	O9plp6 homo sapien	090761 fowlpox vir	Q9j5hl fowlpox vir	Q9su82 arabidopsis	Q9fs13 spinacia ol	Q9su83 arabidopsis	042974 oryza sativ	P90754 caenorhabdi
SUMMARIES		213827	13822	15117	O9R1E6	264610	063490	P97676	P97675	P70641	014638	29NPZ3	29P1P6	090761	29J5H1	Q9SU82	29FS13	Q9SU83	042974	P90754
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,	% Query Match Length DB	100.0	93.3	93.0	88.5	82.8	41.5	41.5	41.5	41.0	40.7	39.0	39.0	22.9	22.9	12.9	12.2	12.2	12.2	12.2
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SECULAT 1 3827 913827 913827 913827 913827 913827 913827 013827 013827 013827 013827 013827 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 16, Last annotation update) AUTOTAXIN.  HORD SAPIENT (AND ALEAZOR) (TREMBLREL) 113 Edwaryotax Metazora; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherais; Primates; Catarrhini; Hominidae; Homo. 11] SEQUENCE FROM N.A. 115 SEQUENCE FROM N.A. 11 SEQUENCE FROM N.A. SEQUENCE FROM N.A. 11 STATE TREMBLRELS (AND ALEA AND AND AND AND AND AND AND AND AND AN										
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01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 16, Last sequence update) 01-NAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) Homo sapiens (Human) Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; MCBL_TAXID-9606; [1] SUBLET EROW N.A. TISSUB-TUMOR; MEDLINE-95074054; PubMed=7982964; MEDLINE-95074054; Andronelogy with phosphodiesterases."; U. Biol. Chem. 269:3047-30484 (1994). EMBL: U3584, AAA64785.1; InterPro: IPR001212: InterPro: IPR001212: InterPro: IPR001212: InterPro: IPR001604; InterPro: IPR001218: IPR0021 SOMATOMEDINB: 2. Pfam: PF01033; SOMATOMEDINB: 2. PRART; SM00477; NUC: 1. SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64; MATCHES 915; CONSETVATIVE NUC: IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	E S	013827	PRELIMINARY;	PRT;	915 AA					
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NAR-2001 (TrEMBLrel. 16, Last annotation update) AUTOTAXIN. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TAXID=9606; [1] SEQUENCE FROM N.A. TISGSTB-TUMOR; MEDLINE-95074054; PubMed=7982964; Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A., Sobel M.E., Liotta L.A., Stracke M.L.; "CDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases."; "CDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases."; TISGSTB, AAA64785.1; InterPro; IPR001212; InterPro; IPR00122; InterPr	텀	01-NOV-1996		Created)						
Ol-MAR-2001 (TrEMBLrel. 16, Last annotation update) AUTOTAXIN. Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TAXID-9606;  (1) SEQUENCE FROM N.A. TISSUE-TUMOR; MUDLINE-95074054; PubMed-7982864; MUTATA.J., Liotta.A., Stracke M.L.; SOBEL M.E., Liotta.L.A., Stracke M.L.; SOBEL M.E., Liotta L.A., Stracke M.L.; SOBEL M.E., Liotta a homology with phosphodiesterases."; J. Biol. Chem. 209:30479-30484(1994). J. Biol. Chem. 209:30479-30484(1994). InterPro: IPR001212; InterPro: IPR001215; InterPro: IPR001215, InterPro: IPR001215; InterPro: IPR001215; INTERPO: IPR001	걾	01-NOV-1996	(TrEMBLrel.	Last sequ	ience ur	odate)				
AUTOTAXIN.  Homo saplens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;  [1]  SEQUENCE FROM N.A.  TISSUE=TUMOR;  MEDLINE=95074054; PubMed=7982964;  MEDLINE=95074054; PubMed=79824(1994).  INTERPRO 1 PROUGL21:  INTERPRO 1 PROUGL21:  PROUGL21:  PROUGL21:  PROUGL21:  PROUGL21:  PROUGL21:  PROUGL21:  PROUGL21:  PROUGL21:  SMART:  SEQUENCE 915 AA: 105246 MW; 2BE6135CCD837780 CRC64;  SEQUENCE 915 AA: 105246 MW; 2BE6135CCD837780 CRC64;  Best Local Similarity 100.0%; Pred. No. 0;  MATCHES 915; CONSETVATIVE O; MISMATCHES PUMUSDSPWTNISGSCK 60  INTERPROPERO PROUGLSTFANCYSICLGFTAHRIKRAEGWEEOPPTVLSDSPWTNISGSCK 60  FILMIHITITITITITITITITITITITITITITITITITITI	占	01-MAR-2001			otation	update	~			
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NCBL_TaxID=9606;  [1] SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE=95074054; PubMed=7982964;  Murata J., Lee H Y., Clair T., Krutzsch H.C., Arestad A.A.,  Sobel M.E., Liotta L.A., Stracke M.L.;  "CDNA -loning of the human tumor motility-stimulating protein,  autotaxin, reveals a homology with phosphodiesterases.";  EMBL: L35544, AAA64785.1;  InterPro: IPR001212;  InterPro: IPR00120591;  InterPro: IPR00120591;  InterPro: IPR001591;  Pfam; PF0103; Somatomedin_B; 2.  Pfam; PF0103; Somatomedin_B; 2.  Pfam; PF0103; Somatomedin_B; 2.  Pfam; PF01052; SOMATOMEDIN_B; 2.  SMART; SM00477; NUC; 1.  SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64;  SEQUENCE 915 AA; 100.0%; Score 5019; DB 4; Length 915;  Best Local Similarity 100.0%; Pred. No. 0;  Aatches 915; Conservative 0; Mismatches 0; Indels 0; Gaps	8	Mammalia; Eu	utheria; Primates		ini; Hc	ominida	е; ношо			
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SEDUENCE FROM N.A.  TISSUE-TUMOR, Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A., Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A., Sobel M.E., Sobel M.	RN	[1]								
TISSUB-TUMOR;  MEDLINE-95074054; PubMed-7982964;  MEDLINE-95074054; PubMed-7982964;  Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A.,  Sobel M.E., Liotta L.A., Stracke M.L.;  Sobel M.E., Liotta L.A., Stracke M.L.;  "CDNA cloning of the human tumor motility-stimulating protein,  autotaxin, reveals a homology with phosphodiesterases.";  J. Biol. Chem. 269:30479-30484(1994).  EMBL: Lis594; AAA64785.1;  InterPro; IPR001212;  InterPro; IPR0012291;  InterPro; IPR001291;  INTERPROSTE; SOMATOMEDIN.B; 2.  SMART; SM00477; NUC; 1.  SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64;  SMART; SM00477; NUC; 1.  SEQUENCE 915 AA; 100.0%; SCOTE 5019; DB 4; Length 915;  Best Local Similarity 100.0%; SCOTE 5019; DB 4; Length 915;  Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps  I MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60	RP	SEQUENCE FRO	OM N.A.							
MEDLINE=95074054; PubMed=7982964; Murata_J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A., Sobel M.E., Liotta L.A., Stracke M.L.; "cDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases."; J. Blol. Chem. 269:30479:30484(1994). EMBL: L35594; AAA64785.1; InterPro: IPR0012012; InterPro: IPR0012012; InterPro: IPR0012012; InterPro: IPR001203; Somatomedin_B; 2. Pfam; PF01033; Somatomedin_B; 2. Pfam; PF01033; Somatomedin_B; 2. PRIMTS: PR00022; SOMATOMEDIN_B; 2. SMART; SM00477; NUC; 1. SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64; SEQUENCE 915 AA; 105046; Pred. No. 0; Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps I MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60	S	TISSUE-TUMOR	3;							
Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A., Sobel M.E.; Sobel M.E.; Sobel M.E.; Sobel M.E.; CDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases."; J. BAOL. Chem. 256:30479-30484(1994). J. BAOL. Chem. 256:30479-30484(1994). InterPro; IPR001212; INTERPROSTITE; PR001212; INTERPROSTITE; PR001212; INTERPROSTITE; PR001212; INTERPROSTITE; PR001212; INTERPROSTITE; PR0111	RX	MEDLINE=9507	74054; PubMed=798	12964;						
Sobel M.E., Liotta L.A., Stracke M.L.;  "CDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases."; J. Biol. Chem. 269:30479-30484(1994).  J. Biol. Chem. 259:30479-30484(1994).  InterPro; IPR001212; InterPro; IPR0012291; InterPro; IPR001291; IPR001013; Somatomedin.B; 2. Pfam; PF01063; PN00477; NUC; InterPro; IPR001291; INCOMATOMEDIN.B; 2. SMART; SM00477; NUC; InterPro; IPR001291; INTERPRO; PR001291; INTERPRO; PR0	RA	Murata J., I	Lee H.Y., Clair T	., Krutzs	ich H.C.	., Ares	tad A.A	:		
"CDNA cloning of the human tumor motility-stimulating protein, autotaxin, reveals a homology with phosphodiesterases."; J. Biol. Chem. 269:30479-30484(1994). EMBL; L35594; AAA64785.1; InterPro; IPR001504; InterPro; IPR001504; InterPro; IPR001504; InterPro; IPR0015051; Pfam; PF01033; Somatomedin_B; 2. Pfam; PF01033; Somatomedin_B; 2. PRINTS; PR00022; SOMATOMEDIN_B; 2. PROSITE; PS00524; SOMATOMEDIN_B; 2. SWART; SM00477; NUC; 1. SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64; SEQUENCE 915 AA; 1050.0%; Pred: No. 0; Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps    MARRSSFQSCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCK 60	RA	Sobel M.E.,	Liotta L.A., Str	acke M.L.						
autocaxin, reveals a homology with phosphodiesterases."; J. Biol. Chem. 269:30479-30484(1994).  EMBL, L35594; AAA64795.1; InterPro; IPR001212; InterPro; IPR001204; InterPro; IPR001204; InterPro; IPR001204; InterPro; IPR001204; InterPro; IPR001205; INTERPOSTITE; INTERO	RŢ	"cDNA clonin	ng of the human t	umor moti	lity-st	timulat	ing prot	tein,		
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
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                                     protein,
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MRDLINE=6518950; PubMed=8579579;
Lee H.Y., Murata J., Clair T., Polymeropoulos M.H., Torres R.
Manrow R.E., Liotta L.A., Stracke M.L.;
"Cloning, chornosomal localization, and tissue expression of ifrom human teratcoarcinoma cells.";
Biochem. Biophys. Res. Commun. 218:714-719(1996).
EMBL: L46720, AAB00855.1;
InterPro; IPR001212; -...
InterPro; IPR001212; -...
Murata J., Lee H.Y., Clair T., Krutzsch H.C., Arestad A.A., Sobel M.E., Liotta L.A., Stracke M.L., "CDNA cloning of the human tumor motility-stimulating prote autotaxin, reveals a homology with phosphodiesterases.";
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PROSTITE; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00477; NUC; 1.
SEQUENCE 863 AA; 99017 WW; F960DCE51663BABC CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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Sano K., Piao J.-H.;
Sano K., Piao J.-H.;
"Cloning and chromosomal assignment of mouse phosphodiesterase
I/nucleotide pyrophosphatase (PD-I alpha/autotaxin).";
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2001 (TrEMBLrel. 16, Last annotation update)
PHOSPHODIESTERASE 1/NUCLEOTIDE PYROPHOSPHATASE (EC.
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MEDLINE-96163899; PubMed-8586446;
Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
Nakamura H., Sano K.;
"Molecular cloning and chromosomal assignment of the human brain-type
phosphodiesterase I/nucleotide pyrophosphatase gene (PDNP2).";
Genomics 30:380-384(1995).
EMBL: D45421; BAA08260.1; -.
InterPro; IPR001212; -.
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Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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PROSITE; PS00524; SOMATOMEDIN_
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01-MAR-2001 (TrEMBLrel. 16,
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InterPro; IPR002591;
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                                                                                                                                                                                                    61 GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 120
                                                                                                                                                                                                               60 GRCFELQEVGPPDCRCDNLCKSYSSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC 119
                                                                                                                                                                                                                                           SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK 180
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                                                                                                                                                                                                                                                                                                                                                                   862;
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 the EMBL/GenBank/DDBJ databases
                                                                                               862 AA; 98918 MW; 641F8F1443E4F8B0 CRC64;
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                                                                                                                         88.5%; Score 4439.5;
88.1%; Pred. No. 0;
                                                                                                                                            30; Mismatches
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                                                         PRINTS; PR00022; SOMATOMEDINB.
PROSITE; PS00524; SOMATOMEDIN_B;
                                     Pfam; PF01033; Somatomedin_B; 2. Pfam; PF01663; Phosphodiest; 1.
Submitted (JAN-1999) to the EMBL; AF123542; AAD46480.1; InterPro; IPR001212; -. InterPro; IPR002591; -.
                                                                                                                                   Best Local Similarity 88.1%
Matches 806; Conservative
                                                                           SMART; SM00201; SO; 1.
Hydrolase.
                                                                                               SEQUENCE
                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Narita M., Goji J., Nakamura H., Sano K.;
"Molecular cloning, expression, and localization of a brain-specific
phosphodiesterase I/nucleotide pyrophosphatase (PD-I alpha) from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC
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                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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llarity 83.6%; Pred. No. 0;
Conservative 33; Mismatches
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EMBL; D28560; BAA05910.1; -.
InterPro; IPR001212; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLINE-95050605; PubMed=7961762;
                                                                                                                                                                                                                                                                               Created)
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PROSITE; PS00524; SOMATOMEDIN_B;
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Hydrolase.
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Sciurognathi; Muridae; Murinae; Rattus
SKHENKKNLNGSVEPRKERHLLYGRPAVLYRTSYDILYHTDFESGYSEIFLMPLWTSYTI
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                                                                                                       NSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTNTFR
                                                                                                                                              PTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLDELNKRLHTKGSTE------
                                                                                                                                                       -------ERHLLYGRPAVLYRTRYDILYHTDFESGYSEIFLMLLWTSYTV
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Last annotation update)
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Pfam; PF01663; Phosphodiest; 1.
PROSITE; PS00524; SOMATOMEDIN_B;
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Q63490;
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Length 875;

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Score 2084;

41.5%;

Query Match

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                                                                                                                                                                                                        279 VIPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRP 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 GSCKGRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEEN 116
                                                                  -----VIKALQLVDDAFGMLMEGLKQR 360
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                                                                                                                                        SYMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDP
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              Indels
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Last annotation update)
9.6e-162;
thes 248;
                                                                                                                                                                                                                                                           237 VFDATFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFW-
              Mismatches
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              Conservative 160;
43.58;
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Similarity
              Matches 386;
Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCSCADDCLQRKDCCTDYKAVCQGEVPWVTEACASSQEPQCPEGFDQPPVILFSMDGFRA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 YLNKNFSLSSVEKSNPAWWSGQPIWLTAMYQGLKAASYYWPGSDVAVNGSFPNIYRNYSN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 VIPHERRILTILRWLTLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRP 338
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                              "Biochemical and molecular identification of distinct forms of alkaline phosphodiesterase I expressed on the apical and basolateral plasma membrane surfaces of rat hepatocytes.";

EMBL; U78788; AAB61536.1; ...
InterPro; IPR001212; ...
InterPro; IPR001212; ...
Pfam; PF0103; Sonatomedin_B; 2.
Pfam; PF0103; Conatomedin_B; 2.
Pfam; PF0103; Conatomedin_B; 1.
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                                                                                                    Goding J.W
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                                                                                                      Trugnan G.,
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                                                                                                                                                                                                                                                                                          PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
                                                                                  MEDLINE=97250927; PubMed=9096610;
Scott L.J., Delautier D., Meerson N.R.,
                                                                                                                                                                                                                                                                                                         SMART; SM00201; SO;
                                                                                                                                                                                                                                                                                                                           875 AA;
                                                                      SEQUENCE FROM N.A.
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Best Local S
Matches 386,
                                                                                                                      Maurice M
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AFLVTNMVPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPIFDYDYDGLHDTEDKIKQ 807
                              Gaps
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                                                                                                             YVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESKW
                                                                                                                                            94;
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Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W
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Interpro; IPR001504; ...
Interpro; IPR002591; ...
Pfam; PF01033; Somatomedin_B; 2.
Pfam; PF01663; Phosphodiest; 1.
PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
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57 GSCKGRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEEN 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 KRKVAPKRRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQL 398
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                                                                                                                    117 ACHCSEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRA
                                                                                                                                                  SYMKKGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AAR-2001 (TrEMBLrel. 16, Last annotation update)
PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE BETA
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                                                                                        KLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIRSK-----FSNN 452
                                                                                                                                                                                                         PAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVEPKNKLD 632
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----VIKALQLVDDAFGMLMEGLKQR 360
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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43.2%; Pred. No. 1.4e-159;
tive 159; Mismatches 251; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE, PROXIMAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sano K.;
"Molecular cloning of phosphodiesterase I cDNA from rat
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Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases
EMBL, D30049, BAA06333.1;
InterPro; IPR001212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| | | |||||:| || |||::: :: ||| ||||| |:|: |
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-RAR-2001 (TrEMBLrel. 16, Last annotation update)
PHOSPHODIESTERASE I.
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Matches 378; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 PVAPPKKRRKKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVG 410
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                                                                      Piao J.-H., Goding J.W., Nakamura H., Sano K.; "Molecular cloning and chromosomal localization of PD-Ibeta (PDNP3), new member of the human phosphodiesterase I genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 40.5%; Pred. No. 3.5e-158;
Matches 379; Conservative 177; Mismatches 268; Indels 111; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 SCQIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCKGRCFELQE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.7%; Score 2040.5; DB 4; Length 875; 40.5%; Pred. No. 3.5e-158;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1999) to the EMBL/GenBank/DpBJ databases.
EMBL; AF005632; AAC51813.1; -.
EMBL; AC005587; AAD5192.1; -.
                                                                                                                                                 Hou S., Wohldmann P., Le T.; "The sequence of Homo sapiens PAC clone DJ0988G15."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                              Waterston R.H.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                              Waterston R.H.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                               875 AA; 100096 MW; 329CF41667497BC4 CRC64;
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                                                           MEDLINE-98008933; PubMed-9344668;
                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01033; Somatomedin_B; 2.
Pfam; PF01663; Phosphodiest; 1.
                                                                                                                                    SEQUENCE OF 189-875 FROM N.A.
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                                                                                                                                                                                                 SEQUENCE OF 189-875 FROM N.A.
                                                                                                            Genomics 45:412-415(1997).
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InterPro; IPR001604;
InterPro; IPR002591;
                                    SEQUENCE FROM N.A.
           NCBI_TaxID=9606;
                                                 TISSUE-PROSTATE;
                                                                                                                                                                                                                                                                                                               Waterston
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                                                                                                                                                                                 DHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNH 585
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                                                                                                                                                                                                                                                                                                                                                                                                                              CKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQG
                                                                                                       LLKVPFYEPSHAEEVSKFSVCGFANPLPTESLDCFC-PHLQNSTQLEQVNQMLNLTQEEI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-0c7-2000 (TrEMBLrel. 15, Last annotation update)
DJ131F15.2 (PHOSPHOLDESTERARE L'NUCLEOTIDE PYROPHOSPHATASE
(HOMOLOGOUS TO MOUSE LY-41 ANTIGEN) (PC1, NPPS)) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peck A.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL117378; CAB99365.1; -.
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Pfam; PF01033; Somatomedin_B; 2.
Pfam; PF01663; Phosphodiest; 1.
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                                                        CHCSEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRAS
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LHRCLNLILISDHGMEQGSCKKYIYLNKYLGDVKNIKVIYGPARLRPSDVPDKYXS---
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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the EMBL/GenBank/DDBJ databases
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PROSTITE; PS00524; SOMATOMEDIN_B;
SMART; SMO0477; NUC; 1.
SEQUENCE 925 AA; 104924 MW; 0
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AAF36094.1;
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InterPro; IPR002591;
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AF110302;
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YTHVSSLDIITIESECDRHARVG-----DHLKGCTCKNIDRFSSKGNKEDSSR---TRS 555
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                                NHRWWGGQPLWITATKQGVKAGTFFW----SVV------IPHERRILTILRW
                                                                                                                                                                  APPKKRRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDH
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Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
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Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock
"The genome of fowDpox virus";
J. Virol. 74:38131(2000).
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01-OCT-2000 (TrEMBLrel. 15, Last seque
01-MAR-2001 (TrEMBLrel. 16, Last annot
ORF FPV030 ALKALINE PHOSPHODIESTERASE.
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-!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
                                                                                                                                                                                                                                                              635 --IEDFQTQFNLTVAEEKIIKHETLPYGRPRVLQKENTICLLSQHQFMSGYSQDILMPLW 692
                                                                                                                                                                                                                     811 ENLRQKRRVIRNQEILIPTHFFIVLTSCKDTSQTPLHCEN-LDTLAFILPHRTDNSESCV 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKF 250
515 KKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPA 574
                  575 PNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDF-----DLGCTCDDKVEPK 628
                                                                                  NKLDELNKRLHTKGSTEE--RH--LLYGRPAVLYR-TRYDILYHTDFESGYSEIFLMLLW 683
                                                                                                                                                                                                   TSYTVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCLAYKNDKQMSYGFLFPPYLSSSPE 743
                                                                                                                                                                                                                                                                                                                                 803 DKIKQ---YVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCN 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 CTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                 860 SSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPEILTLKTYLHTYESE 914
                                                                                                                                                                                                                                                                                                                                                                                                                     870 HGKHDSSWVEELLMIHRARITDVEHITGLSFYQQRKEPVSDILKLKTHLPTFSQE 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.9%; Score 1151; DB 14; Length 817; Best Local Similarity 32.4%; Pred. No. 1.9e-85; Matches 263; Conservative 141; Mismatches 276; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE)
NUCLEOTIDE PHOSPHODIESTERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94004 MW; CB68DA0508CC568E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01663; Phosphodiest; 1.
SMART; SM00477; NUC; 1.
FAUTOLIASE 817 AA; 94004 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ006408; CAA07014.1;
InterPro; IPR001604; -.
InterPro; IPR002591; -.
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NCBI_TaxID=10261;
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                                                                                                                                                                       KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKF 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SFQDWTAVFLGYGPAFLDDVRVPIFDNIELYNMMCEILGINPANNNGTVGSLNNILRNSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTHVSSLDIITIESECDRHAYG-----DHLKGCTCKNIDRFSSKGNKEDSSR---TRS
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                                                                                                                                                                                                                                      NHRWWGGQPLWITATKQGVKAGTFFW----SVV------IPHERRILTILRW
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                                                                                                                                                                                                                                                                                                                353 APPKKRRKIHRMDHYAAETRQDKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDH
                                                                                                                      Query Match 22.9%; Score 1151; DB 14; Length 817; Best Local Similarity 32.4%; Pred. No. 1.9e-85; Matches 263; Conservative 141; Mismatches 276; Indels 132;
 EMBL/GenBank/DDBJ databases
                                                                                             8404FD00641DA022 CRC64;
                                                                                                                                                                                                                                                                                             LKMDTGYRPYFYALYLEEPGSSGYEYG------
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         EMBL; AF198100; AAF44374.1;
InterPro; IPR001428; -.
Submitted (OCT-1999) to
                                      IPR002591; -.
                             IPR001604;
                            InterPro;
                                     InterPro;
                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 TKQGVKAGTFFW--------SVVIPHERRILTILRWLTLPDHERPSV 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 RMDHYAAETRODKMTNPLREIDKIVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 FLSNYLTHVVDDITLVPG-----TLGR-IRSKFSNNAKYDPKAIIANLTCKK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 DDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIEKLRSCGTHSPY-MRP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 VYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKFNHRWWGGQPLWITA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 646.5; DB 10; Length 457;
32.0%; Pred. No. 1.5e-44;
Live 78; Mismatches 136; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mewes H.W.,
                                                                                                                                                                                                              Arabioopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brasslcales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 DSPSSYVRRPQPPKKLNKPVVLLISCDGFRFGYQFKTE--TPNIDLLISRGTEAKTGLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 VNQGLMAATYFWPGADVHKGSWNCPKGFCKAPYNVSVPLEERVDTILNYFDLPEREIPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::| ::||::||:|| ||:
------RVTEAVSKVDKMIGRIIMGLEKRKVFSDVHVILLGDHGMV-TNCDKKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bevan M., Rose M., Hempel S., Entian K.-D., Bancroft I.,
Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO/934; CAB45329.1; -.
EMBL; ALO/1575; CAB79727.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 AA; 51261 MW; 3B95E6C0AE1B1215 CRC64;
                                                                  01-OCT-2000 (TrembLrel. 13, Last sequence update)
NUCLEOTIDE PYROPHOSPHATASE-LIKE PROTEIN (EC 3.6.1.9)
TIGL4.200 OR AT4G29690.
457 AA
                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2000 (TrEMBLrel. 15, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01663; Phosphodiest; 1.
Hydrolase.
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PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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528 GFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMCDLLGLKPAPNNGT 579

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Search completed: July 19, 2001, 14:46:48 Job time: 171 sec

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Autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; addipocyte; hypoglycemic; antidiabetic; antidiabetic; attilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPses; adenosine-5'-triphosphatase activity; phosphodiesterase catalytic site.
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                                  AAR86595
AAR86595
AAX83620
AAX83621
AAX83621
AAX83621
AAX831321
AAG29473
AAG31321
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AAG39473
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AAW01573
AAX84037
AAB53329
AAW40378
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AAY34324
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AAW52839
AAY17529
AAY02378
AAB90545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY71992 standard; peptide; 13 AA
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 WPI; 2001-007397/01
WO200068386-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
AAY71992
   Rat autotaxin prot
Rat autotaxin vari
Rat autotaxin vari
Rat autotaxin vari
Rat autotaxin vari
Human autotaxin pr
Human teratocarcin pr
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Autotaxin derived
                                                                                                                                           (without alignments)
22.745 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                      July 19, 2001, 14:45:00 ; Search time 34.65 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                     Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     412676 seqs, 60623988 residues
                                                                                                                                                                                  US-09-483-831-69_COPY_201_213
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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AAR86579
AAR86578
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AAY71995
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AAY71997
AAY71998
AAY71999
AAY71991
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                             1 YMRPVYPTKTFPN 13
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Maximum DB seq length: 200000000
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Score

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                                                                           The present sequence is autotaxin phosphodiesterase catalytic site. Phosphorylation of threonine residue at position 10 of this sequence is required for autotaxin to undergo autophosphorylation and exhibit phosphodiesterase and motility-stimulating activities. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Autotaxin derived from teratocarcinoma N-tera 2D1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 76; DB 22;
; Pred. No. 1.8e-06;
0; Mismatches 0;
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                                                 Disclosure; Page 3; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR86579 standard; Protein; 788 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                    human metabolic diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YMRPVYPTKTFPN 13
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                                                                                                                                                                                                                                                                                                                                                                                                  13 AA;
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AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is

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                                                         transmembrane bound form is not present in tumour cells. The CDNA encoding this sequence can be used in a vector, to transform cells. The crombinant cells can then be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXT, while having little effect on the membrane form of AXT.
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                                                                                                                                                                                                                                                                                                                                                             Gaps
an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. The tumourous form of ATX is a secreted protein, while the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stimulating protein, and DNA encoding it · used
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                                                                                                                                                                                                                                                                                                                   100.0%; Score 76; DB 17; 100.0%; Pred. No. 0.00012;
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                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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in cancer diagnosis and therapy
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94US-0249182.
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                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                               788 AA;
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Indels

Length 858;

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signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (APPASS) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, ipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New autotaxin proteins, useful e.g. for treating diabetes mellitus obesity, stimulate glucose uptake by cells and inhibit lipolysis \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is variant (A93V) of rat autotaxin protein. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type Ala substituted by Val"
                                                                                                                                                                                                                                                                                                                    100.0%; Score 76; DB 22;
100.0%; Pred. No. 0.00014;
tive 0; Mismatches 0;
 glycoprotein cytokine which increases insulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71995 standard; Protein; 858 AA.
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                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 13; Conserv
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This region is absent in rat brain autotaxin designated
as PD-Ialpha sequence (AAY71989)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Epitope
/note= "This region is specifically claimed in claim 10"
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                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adjocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity.
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                                                                                         Length 829;
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                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Putative transmembrane domain"
                                                                                         DB 17;
0.00013;
thes 0;
having little effect on the membrane form of AXT
                                                                                           Score 76; DB
Pred. No. 0.00
; Mismatches
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Best Local Similarity
Matches 13; Conserv
                                    829 AA;
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ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
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obesity, stimulate glucose uptake by cells and inhibit lipolysis
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Best Local Similarity
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gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free farty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.

Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAY71986).
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obesity, stimulate glucose uptake by cells and inhibit lipolysis
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100.0%;
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858 AA; Seguence

100.0%; Score 76; DB 22; 100.0%; Pred. No. 0.00014; ative 0; Mismatches 0; Conservative 1 YMRPVYPTKTFPN 13 Query Match Best Local Similarity Matches 13; Conserv g ò

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Gaps

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Indels

Length 858;

AAY71998 standard; Protein; 858 AA. Rat autotaxin variant (R265K). (first entry) 28-MAR-2001 AAY71998; œ AAY71998 ID AAY7 

Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatuse activity; ATP asse; adenosine-5'-triphosphatase activity; mutant; muteni; variant.

Rattus sp. Synthetic.

Location/Qualifiers Misc-difference 265

/note= "Wild type Arg substituted by Lys"

WO200068386-A1

16-NOV-2000

05-MAY-2000; 2000WO-US12402.

99US-0306979. 07-MAY-1999;

(ZYMO ) ZYMOGENETICS INC

Kelly JD;

WPI; 2001-007397/01.

New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -

Disclosure; Page -; 126pp; English.

The present sequence is variant (R265K) of rat autotaxin protein. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic

ö New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis  $\cdot$ gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.
Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases. Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant. Gaps The present sequence is variant (\$289T) of rat autotaxin protein. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by roducing substrate for adenosine receptors, resulting in inhibition of lipplysis, decreased hepatic ö Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in Length 858; /note- "Wild type Ser substituted by Thr" 0; Indels 100.0%; Score 76; DB 22; 100.0%; Pred. No. 0.00014; tive 0; Mismatches 0; page 101-104 of sequence listing (AAY71986) Location/Qualifiers AAY71999 standard; Protein; 858 AA. Disclosure; Page -; 126pp; English. Rat autotaxin variant (S289T). 05-MAY-2000; 2000WO-US12402. (first entry) Conservative (ZYMO ) ZYMOGENETICS INC 196 ymrpvyptktfpn 208 13 WPI; 2001-007397/01. Query Match Best Local Similarity Matches 13; Conserv 1 YMRPVYPTKTFPN 858 AA; Misc-difference WO200068386-A1 07-MAY-1999; 28-MAR-2001 16-NOV-2000 Rattus sp. Synthetic. Kelly JD; Sequence AAY71999; AAY71999 RESULT 266666666666666888 ò

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AAY71988
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gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.
Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
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123.125
7/label- RGD_binding_domain
197.209
/note= "Putative phosphodiesterase active site"
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8..26
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Best Local Similarity
                                                                                                                                                                                                                                                                                                         858 AA;
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                                                                                                                                                                                                                                                                                                              Sequence
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The present sequence is human autotaxin protein.

Autotaxin is a glycoprotein cytokine which increases insulin signaling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-criphosphatase (ArPase) and ATP pyrophosphatase activities.

Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgemic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; teratocarcinoma.
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Pred. No. 0.00014;
Mismatches 0;
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/label= RGD_binding_domain
201..213
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859 AA;
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               teratocarcinoma cells. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in Inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF; melanoma cell; tumour; antibody; cancer diagnosis; therapy.
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                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 76; DB 22; Length 863; 100.0%; Pred. No. 0.00014; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Autotaxin motility stimulating protein, and DNA encoding it in cancer diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stracke M;
   present sequence is autotaxin isolated from human
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94US-0249182
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                             human metabolic diseases
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                                                                                                                                                                                                                                                                                                 863 AA;
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Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXT, while having little effect on the membrane form of
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is autotaxin isolated from human melanoma cells. Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatase activities. Autocaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, autotaxin, lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodisterase activity; AFP pyrophosphatase activity; AFP prophosphatase activity; AFP prophosphatase activity; melanoma.
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                                                                                                                                                                                            Indels
                                                                                                                                                          100.0%; Score 76; DB 17;
100.0%; Pred. No. 0.00015;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human melanoma autotaxin.
                                                                                                                                                                                            Conservative
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                                                                                                                                                    Query Match
Best Local Similarity
Matches 13; Conser
                                                                                                         915 AA;
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                                                                                                         Sequence
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AAR86559-R86596 represent autotaxin (ATX) and fragments of it.
                      Claim 4; Page 67-70; 112pp; English.
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or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for
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                                                                                                                                                                               Length 915;
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                                                                                                                                                                                                                          Indels
                                                                                                                                                                            Score 76; DB 22;
Pred. No. 0.00015;
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Misc-difference 889
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Misc-difference 975
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                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Autotaxin derived from human liver cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                        Conservative
                                                                    human metabolic diseases
                                                                                                                                                                                                                                                                                         Liotta L,
                                                                                                                                                                                                                                                                   1 YMRPVYPTKTFPN 13
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                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                             915 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanoma cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9532221-A2
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                                                                                                               Sequence
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an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. ATX stimulates both random and directed migration of melanoma transmembrane bound form is not present in tumour cells. The cDNA encoding this sequence can be used in a vector, to transform cells. The recombinant cells can then be used in a vector, to transform cells. The haribodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXT, while
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF; melanoma cell; tumour; antibody; cancer diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 76; DB 17; Length 979; 100.0%; Pred. No. 0.00016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stracke M;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                           having little effect on the membrane form of AXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murata J, Schiffmann E,
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 86-89; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR86595 standard; Protein; 849 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-tera 2D1 autotaxin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US06613.
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94US-0249182.
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                            979 AA;
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sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXT, while having little effect on the membrane form of AXT.
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Sequence 849 AA;

; 0 Gaps ; ; Query Match
93.4%; Score 71; DB 17; Length 849;
Best Local Similarity 92.3%; Pred. No. 0.00091;
Matches 12; Conservative 1; Mismatches 0; Indels

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QQ

Search completed: July 19, 2001, 14:45:00 Job time: 208 sec

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TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEC ID NO: 36
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                US-08-346-455B-36
                                                              July 23, 2001, 13:16:07; Search time 20.3 Seconds (without alignments) 12.901 Million cell updates/sec
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Sequence 34,
Sequence 69,
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Sequence 67,
Sequence 67,
Sequence 67,
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Sequence 36,
Sequence 36,
Sequence 34,
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Sequence 6
Sequence 3
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                                                                                                                                                                                                                                                                                                                                 1: ./cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US95-06613-36
US-08-37-21-34
PCT-US95-06613-34
US-08-97-221-69
PCT-US95-06613-34
US-08-97-221-69
PCT-US95-06613-69
US-08-97-221-69
US-08-97-221-67
US-08-97-221-67
US-08-97-221-67
US-08-97-221-67
US-08-97-221-67
US-08-97-221-67
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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US-08-504-169-1
                                                                                                                                                                                            193259 seqs, 20144635 residues
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76
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                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                    1 YMRPVYPTKTFPN 13
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Maximum DB seq length: 200000000
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Match Length DB
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220, Appl
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120, App
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20, Appl
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18, Appl
118, Appl
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Sequence 2
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Sequence 5
Sequence 8
Sequence 8
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Patent No. 5731167
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                    US-07-865-166A-6
US-08-207-481-20
PCT-US95-02689-20
US-08-481-985B-120
US-08-370-476-120
US-08-370-476-120
US-08-080-25-8
US-08-080-25-8
US-08-080-25-8
US-08-08-08-10-20
US-08-09-64-20
US-08-560-388-10
US-08-560-388-10
US-08-560-388-10
US-08-560-388-10
US-08-560-388-10
US-08-528-122-18
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Wordferfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: DOROTHY R. AUTH
REGISTRATION UNDHER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
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TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
SEQUENCE CHARACTERISTICS: LENGTH: 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YMRPVYPTKTFPN 13
                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                    ORGANISM: Human
                                                                                                             HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                            LOCATION
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US-08-977-221-36
Sequence 36, Application US/08977221
Fatent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
STATE: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 76; DB 1; Length 788; 100.0%; Pred. No. 0.00011;
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COTHER INFORMATION: ATX protein sequence US-08-346-455B-36
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 08/249,182
FILING DATE: 17-JAN-1994
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                TISSUE TYPE:
CELL TYPE: teratocarcinoma
CELL LINE: N-tera 2D1
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
                                                                                                DEVELOPMENTAL STAGE
                                                                            INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEW YORK
                                        ORGANISM: Human
     HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                            ORGANELLE:
                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                   HAPLOTYPE
                                                                                                                                                                                                                                                  LOCATION:
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LEMCHINE 788

STRANDENESS: SINGLE

ORGANISS: SINGLE

ORGANISS: SINGLE

ORGANISS: SINGLE

ORGANISS: SINGLE

ORGANISS: Broan

INDIVIDADLA ISOLARE:

DEALTH STRANDEN STACE:

ORGANISH: Broan

STRANDEN STACE:

ORGANISH: Broan

STRANDEN STACE:

DEALTH STRUCKLYOR WENDO:

OTHER INCOMPATION: N'-tera 2D1 putative

OTHER INCOMPATION:
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Patent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HELLTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 76; DB 1; I 100.0%; Pred. No. 0.00012;
               PELING APPLICATION DATA:

APPLICATION NUMBER: 07/822,043
FILING DATE: 17-3N-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36 434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 759-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORGPEFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
    FILING DATE: 25-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE: Melanoma CELL LINE: A2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 YMRPVYPTKTFPN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-346-455B-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANELLE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-977-221-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-346 455B-34

US-08-346 455B-34

Sequence 34, Application US/08346455B

Patent No. 5731167

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.

APPLICANT: OF HEALTH AND HUMAN SERVICES

TITLE OF INVENTION: MOTILITY STIMULATING

TITLE OF INVENTION: THERAPY

TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 76; DB 5; I 100.0%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
COTHER INFORMATION: N-tera 2D1 putative
COTHER INFORMATION: ATX protein sequence
PCT-US95-06613-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 758-4849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE: teratocarcinoma CELL LINE: N-tera 2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                      MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 YMRPVYPTKTFPN 138
                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                       788
                                                                                                                                                                                                                                                                                                                                                                                          HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24 -MAY-1995
CLASSIFICATION:
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-346-455B-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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PCT-US95-06613-34
; Sequence 34, Application PC/TUS9506613
; Sequence 34, Application PC/TUS9506613
; GENERAL IMPORMATION:
    APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
    APPLICANT: SHIFFMANN, ELLIOTT; KRUTZSCH,
    APPLICANT: HENRY; MOTALATA, JUN
    TITLE OF INVENTION: MOTILITY STIMULATING
    TITLE OF INVENTION: THERAPY
    NUMBER OF SEQUENCES: 69
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: MORGAN & FINNEGAN
    STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 76; DB 3; Length 829; conservative 0; Mismatch.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Putative protein
OTHER INFORMATION: sequence of A2058 Autotaxin
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 07/822,043
APPLICATION NUMBER: 07/822,043
ATTORNEY AAGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 2026-4149US3
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34:
SEDENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE: Melanoma
CELL LINE: A2058
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YMRPVYPTKTFPN 13
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SITRET: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 10154
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Patent No. 5731167
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDING ADDRESSES:
ADDRESSES: WORGAN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Putative protein CTHER INFORMATION: sequence of A2058 Autotaxin PCT-US95-06613-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 76; DB 5; I
100.0%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                       NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
RECESTRENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATOMNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 758-4800
TELEFRAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 34
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/977,221
                                                                                                                           PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-414
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: A2058 ATX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 758-4800
TELEFRAX: (212) 751-6849
INFORMATION FOR SEO ID NO: 69;
SEQUENCE CHARACTERISTICS:
    Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
COTHER INFORMATION:
US-08-977-221-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-977-221-69
Subsequence 69, Application US/08977221
Fatent No. 6084069
GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: UNITED STATES OF AMERICA; DEPT.
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS: 69
CORRESPONDENCE ADDRESS: 69
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 76; DB 1; Length 915; 100.0%; Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                        ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FlOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION NUMBER: US/08/346,455B
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 36,434
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
MAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 36,4300
TELEFONNINICATION INFORMATION:
TELEFONNINICATION INFORMATION:
TELEFONNINICATION FOR SEQ ID NO: 69:
SEQUENCE:
AUGUSTANION FOR SED ID NO: 69:
SEQUENCE:
AUGUSTANION FOR SED ID NO: 69:
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36,434
эв. 2026-4149РСТ
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Matches 13; Conservative
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COTHER INFORMATION:

US-08-346-455B-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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U.S.A.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

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RESULT 9
PCT-US95-06613-69
Sequence 69, Application PC/TUS9506613
GENERAL INFORMATION.
APPLICANT: STRACKE,
APPLICANT: SCHIFFMANN, ELLIOTTA, LANCE;
APPLICANT: HENRY: MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 1345 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
                                  ö
100.0%; Score 76; DB 3; Length 915; 100.0%; Pred. No. 0.00013;
                                  0; Indels
                                  0; Mismatches
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US-08-977-21-38

US-08-977-21-38

Sequence 38, Application US/08977221

Patent No. 6084069

GENERAL INFORMATION:

APPLICANT: UNITED STATES OF AMERICA; DEPT.

APPLICANT: OF HEALTH AND HUMAN SERVICES

TITLE OF INVENTION: POTILITY STIMULATING

TITLE OF INVENTION: PROTEIN USFUL IN CANCER DIAGNOSIS AND

TITLE OF INVENTION: PROTEIN USFUL IN CANCER DIAGNOSIS AND

TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 76; DB 1; Length 979; 100.0%; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : putative autotaxin
: protein sequence from human liver
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/82,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 751-6449
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: NEW YORK
CONTRY: U.S.A.
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OMPOTER: IBM PC Compatible
OFFRATING SYSTEM: PC-DOS/MS-DK
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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OTHER INFORMATION: pu
OTHER INFORMATION: pr
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-346-455B-38

Sequence 38, Application US/08346455B

Sequence 393, Application US/08346455B

GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: UNITED STATES OF AMERICA; DEPT.
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES:
OCRESPONDENCE ADDRESS:
ADDRESSEE: 09
CORRESPONDENCE ADDRESS:
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 76; DB 5; Length 915; 100.0%; Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                     PULICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-00v-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 28-MAY-1994
FILING DATE: 27-MAY-1994
FILING DATE: 17-MAY-1992
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: 264,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-1994
18: 530
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
         APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: A2058 ATX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; IDENTIFICATION METHOD:
; OTHER INFORMATION:
PCT-US95-06613-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
: U.S.A.
                                   FILING DATE: 2. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U. ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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Indels

0; Mismatches

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Gaps
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Sequence 67, Application US/08346455B

Sequence 67, Application US/08346455B

PATCH NO. 5731167

APPLICANT: UNITED STATES OF AMERICA; DEPT.

APPLICANT: OF HEALTH AND HUMAN SERVICES

TITLE OF INVENTION: MOTILITY STIMULATING

TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND

TITLE OF INVENTION: THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: putative autotaxin
OTHER INFORMATION: protein sequence from human liver
PCT-US95-06613-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 76; DB 5; I
                                                                                                                                                                                                                                                                                            PRIOR PARLICATION DATA:
APPLICATION NUMBER: 08/346,455
APPLICATION NUMBER: 08/346,455
PRILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US2
TELECOMMUNICATION INFORMATION:
TELEFONDE: (212) 751-6849
INFORMATION FOR SEQ. ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                  PCT/US95/06613
                              COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                           24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                 FILING DATE: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
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PGT-0295-06613-38
Sequence 38, Application PC/TUS9506613
Sequence 38, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY: LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
CORRESPONDENCE ADDRESS: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 76; DB 3; Length 979; 100.0%; Pred. No. 0.00014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
DENTIFICATION METHOD:
COTHER INFORMATION: putative autotaxin
COTHER INFORMATION: protein sequence from human liver
US-08-977-221-38
                                                                                                          PUCASSIFICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTONBEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REGISTRATION NUMBER: 36,434
RECISTRATION NUMBER: 36,434
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
TISSUE TYPE: Liver
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 YMRPVYPTKTFPN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANELLE:
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NAME/KEY:
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PESULT 15
PCT-US95-06613-67
PCT-US95-06613-67
SEQUENCE 67, Application PC/TUS9506613
GENERAL INFORMATION:
APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZSCH,
APPLICANT: HENRY; MURATA, JUN
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.4%; Score 71; DB 3; Length 861; 92.3%; Pred. No. 0.00079; rive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: DOROTHY R. AUTH
REGISTRATION NONBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPRAX: (212) 754-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 67:
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: N-tera 2D1 ATX protein
                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MOTILITY STIM
TITLE OF INVENTION: PROTEIN USEFU
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: GO
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.4
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION:
US-08-977-221-67
U.S.A.
                                                                                                                                                                                                                                                                                             FILING DATE:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              á
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Patent No. 6084069

GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
APPLICANT: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.4%; Score 71; DB 1; Length 861
92.3%; Pred. No. 0.00079;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: WORDPErfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,455B
FILING DATE: 28-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/06613
FILING DATE: 24-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/829,182
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 2026-4149PCT
TELECOMMUNICATION INFORMATION:
TELEFONDE: (212) 756-4800
TELEFONDE: (212) 756-4800
TELEFONDEC: CLASSION OF 575-6849
INFORMATION FOR SEQ 1D NO: 67:
SUMMER: OFFICENCE OF 15 DECTATION OF 15 DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: N-tera 2D1 ATX protein
                       ADDRESSEE: MORGAN & FINNE
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.4
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YMRPVYPTKTFPN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION:
US-08-346-455B-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEW YORK
NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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Search completed: July 23, 2001, 13:22:06 Job time: 359 sec

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0; Gaps

93.4%; Score 71; DB 5; Length 861; 92.3%; Pred. No. 0.00079; tive 1; Mismatches 0; Indels

Query Match 93.4 Best Local Similarity 92.3 Matches 12; Conservative

1 YMRPVYPTKTFPN 13 :||||||||||||||| 201 HMRPVYPTKTFPN 213

δ

Tue Jul 24 10:41:09 2001

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein July 19, 2001, 14:45:54; Search time 25.97 Seconds (without alignments) 38.131 Million cell updates/sec Run on:

US-09-483-831-69\_COPY\_201\_213 76 1 YMRPVYPTKTFPN 13 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pirl:\* pir2:\* pir3:\* pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Length	BB	A	Description
-	92	100.0	915	-	A55144	autotaxin precurso
7	70	92.1	882	Н	A55453	plasma celî membra
m	69	8.06	96	7	A25274	phosphodiesterase
4	69	8.06	300	~	A41179	protein kinase PC-
5	69	8.06	925	Н	A39216	plasma cell membra
9	99	86.8	905	-	A27410	
7		85.5	875	Н	A57080	cell surface antig
80	54	71.1	493	~	S50443	
σ	20	65.8	743	7	S19437	
10	49	64.5	457	ď	T09932	>
11	49	64.5	461	7	T09933	nucleotide pyropho
12	49	64.5	829	7	T19494	hypothetical prote
13	48	63.2	496	7	T09931	
14	47	61.8	479	~	T03293	nucleotide pyropho
15	45	59.5	674	7	T19495	hypothetical prote
16	44.5	58.6	316	~	S46237	г
17	42		429	~	T33724	hypothetical prote
18	41		247	~	T32514	
19	41	53.9	381	~	T23250	
20	41	•	427	~	S57776	cysteine proteinas
21	41	w.	433	~	B82537	phosphodiesterase-
22	41	٠.	493	~	T01206	cysteine proteinas
23	41	ë.	1829	~	T24583	hypothetical prote
24	40	52.6	174	~	S15391	crustacyanin chain
25	40	3	202	~	G01942	mitotic feedback c
56	40		247	N	T45847	hypothetical prote
27	40	'n	346	N	JA0159	cysteine proteinas
28	40	ς.	466	~	T06416	Ū
53	40	52.6	1547	~	J00096	

probable embryo-ab hypothetical prote hypothetical prote aminoacid carrier probable phophodie hypothetical prote outer membrane pro serine/threonine-s Myb DNA binding pr hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote	hypothetical prote probable outer mem serotype-1-specifi
A84841 E86423 T16795 G69809 T40657 F64580 F64580 F749254 C52687 C72698 C72698 S24760	139924 E81965 H81020
0000000000000	0000
269 321 451 471 528 1064 256 453 567	791 1068 1082
00000000000000000000000000000000000000	20.0 20.0 20.0
<b>ᲗᲗᲗᲗᲗᲗᲗᲗᲗᲚᲚᲚ</b> ᲝᲝᲝᲝᲝᲝᲝᲝᲝᲝᲝ	9888
33333333333333333333333333333333333333	4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

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C;Accession: A55144; A42329
R;Murata, J.; Lee, H.Y.; Clair, T.; Krutzsch, H.C.; Arestad, A.A.; Sobel, M.E.; Liott
J. Biol. Chem. 269, 30479-30484, 1994
A;Title: cDNA cloning of the human tumor motility-stimulating protein, autotaxin, rev
A;Reference number: A55144; MUID:95074054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-915 <MUR>
A; Residues: 1-915 <MUR>
A; Residues: 1-915 <MUR>
A; Residues: 1-915 <MUR>
A; Residues: 1-916 <MUR>
A; Note: parts of this sequence were confirmed by peptide sequencing
B; Stracke, M.L.; Krutzsch, H.C.; Unsworth, E.J.; Arestad, A.; Cioce, V.; Schiffmann, J. Biol. Chem. 267, 2524-2529, 1992
A; Title: Identification, purification, and partial sequence analysis of autotaxin, a A; Reference number: A42329; MUID:92129337
                              N:Contains: phosphodiesterase I (EC 3.1.4.1)
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
autotaxin precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A55144
```

A; Accession: A42329

A; Molecule type: protein
A; Residues: 256.266;422-444;504-507,'AN';510,'X',511-515;533-548;'S',554-559,'N',561A; Residues: 256-266;422-444;504-507,'AN';510,'X',511-515;533-548;'S',554-559,'N',561A; Residues: A208 melanoma cells
A; Note: sequence extracted from NCBI backbone (NCBIP:78526, NCBIP:78523, NCBIP:78521,
A; Note: a peptide fragment Tyr-Asp-Val-Pro-Trp-Asn-Glu-Thr-Ile was also found
C; Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.

C,Genetics: A,Gene: GDB:ATX A,Cross-references: GDB:378346

A Map position: 8422-8qter C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology C; Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase F; 55-98/Domain: somatomedin B homology <SBH1> F; 54,463,577,859/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 210/Binding site: AMP (Thr) (covalent) #status predicted

Gaps ö 100.0%; Score 76; DB 1; Length 915; 100.0%; Pred. No. 5.8e-05; Indels Mismatches ó Query Match 100. Best Local Similarity 100. Matches 13; Conservative

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1 YMRPVYPTKTFPN 13 ð

a

RESULT A55453

plasma cell membrane glycoprotein PC-1, brain specific - rat N;Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)

```
protein kinase PC-1 (EC 2.7.1.-) - bovine (fragments)

N.Alternate names: MAPP: major acidic fibroblast growth factor-stimulated phosphoprot C; Species: Bos primiquenius taurus (cattle)
C; Date: 28-May-1992 #sequence_revision 22-Apr-1995 #text_change 30-Apr-1999
C; Accession: A41179; A49308
R; Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 266, 16791-16795, 1991
A; Title: The plasma cell membrane glycoprotein, PC-1, is a threonine-specific protein A; Recerence number: A41179; MUID:91358477
A; Accession: A4179
A; Molecule type: protein
A; Receius: 1-26; 86-65; 59-67; 68-133; 134-144; 145-267; 268-300 <ODA>
A; Experimental source: liver
B; Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 268, 27318-27356, 1993
A; Title: The major acidic fibroblast growth factor (aFGF)-stimulated phosphoprotein festerase activities.
A; Receius: 27-35, 73-58 < COD2>
A; Reperimental source: liver
A; Molecule type: protein
A; Residues: 27-35, 73-58 < COD2>
A; Reperimental source: liver
A; Molecule type: protein
A; Residues: 27-35, 73-58 < COD2>
A; Reperimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIP:141583)
C; Superimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIP:141583)
C; Superimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIP:141583)
C; Superimental source: liver
A; Note: sequence extracted from NCBI backbone (NCBIP:141583)
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A; Note: sequence extracted from NCBI backbone (NCBIP:141583)
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A; Note: sequence extracted from NCBI backbone (NCBIP:141583)
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R;Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Hori, Y.; Kobayashi, H.; Inoue, T.; S
Arch. Biochem. Biophys. 295, 180-187, 1992
A;Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase. A;Reference number: S21706; MUID:92246539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.Contains: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.4.1)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: 10-59p-1999 #sequence.25equence.
C.Species: A39216; S21706; S25891; S51030
R.Buckley, M.F.; Loveland, K.A.; McKinstry, W.J.; Garson, O.M.; Goding, J.W.
J. Blol. Chem. 265, 17506-17511, 1990
A;Title: Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule, A;Reference number: A39216; MUID:91009202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A;Residues: 116-121;247-271,'X',273-275;279-280,'X',282-283;303-316;362-364;449-465;4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Belli, S.I.; Goding, J.W.
Eur. J. Biochem. 226, 433-443, 1994
A;Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score 69; DB 2; I
Pred. No. 0.00029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.8%; Score 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
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A; Residues: 1-925 <FUNI>
A; Accession: S23587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-925 <BUC>
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A. Residues: 1-885 - CNARA
A. Residues: 1-885 - CNARA
A. Cross-references: GB1D28560; NID:9464196; PIDN:BAA05910.1; PID:9464197
B. A. Cross-references: GB1D28560; NID:9464196; PIDN:BAA05910.1; PID:9464197
B. R. Residues: 1-60.10 J.; Sano, K.; Nakamura, H.
Submitted to JIPID, February 1994
A. Description: Cloning and expression of brain-specific nucleotide diphosphohydrolase.
A. Reference number: JU0187
A. Recession: JU0187
A. Recission: JU0187
A. Residues: 1-66, Q', 68-81, Tr, 83-94, 'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66, Q', 68-81, Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66, Q', 68-81, Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66, Q', 68-81, Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 68-81,'Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 68-81,'Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 68-81,'Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 68-81,'Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 68-81,'Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 68-81,'Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 68-81,'Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 68-81,'Tr, 83-94,'C', 96,'A', 98-195,'A', 197-514,'E', 516-621,'E', 623-6
A. Residues: 1-66,'Q', 8-10, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109, 100-109,
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A;Residues: 1-61 <CUL>
R;Maruyama, E.; Iwamatsu, A.; Takashima, S.
Biochem. Mol. Biol. Int. 29, 579-586, 1993
A;Title: Purification and amino acid microsequencing of alkaline phosphodiesterase I frc
A;Reference number: A48395; MUID:93250579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphodiesterase I (EC 3.1.4.1) - bovine (fragments)
N;Alternate names: 5'-exonuclease
N;Alternate names: 5'-exonuclease
S;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1988 #sequence_revision 23-Mar-1995 #text_change 21-May-1999
C;Accession: A25274; C48395; A48395; D48395
R;Culp, J.S.; Blytt, H.J.; Hermodson, M.; Butler, L.G.
J. Biol. Chem. 260, 8320-8324, 1985
A;Title: Anino acid sequence of the active site peptide of bovine intestinal 5'-nucleoti
A;Reference number: A25274; MUID:85234541
                            C;Date: 10.Sep-1999 #sequence_revision 10.Sep-1999 #text_change 16-Jun-2000 C;Accession: A55453; JU0187 Erevision 10.Sep-1999 #sequence_revision 10.Sep-1999 #sequence_revision 10.Sep-1999 #text_change 16-Jun-2000 C;Accession: A;Goji, J.; Nakamura, H.; Sano, K. J. Biol. Chem. 269; 28235-28242, 1994 A;Title: Molecular cloning, expression, and localization of a brain-specific phosphodies A;Reference number: A55453; MUID:95050605
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A;Residues: 22-36,62-73;74-81;82-96 <WAR>
A;Experimental source: kidney
A;Note: sequence extracted from NCBI backbone (NCBIP:132415, NCBIP:131478)
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Pred. No. 0.00058;
0; Mismatches 1
C;Species: Rattus norvegicus (Norway rat)
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
Matches 11; Conserv
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R;Deissler, H.; Lottspeich, F.; Rajewsky, M.F.
J. Biol. Chem. 270, 9849-9855, 1995
A;Title: Affinity purification and cDNA cloning of rat neural differentiation and tum A;Reference number: A57080; MUID:95247775
A;Seference number: A57080
A;Status: preliminary
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F;206/Binding site: AMP (Thr) (covalent) #status predicted
F;237,280,289,533,574,594,702,789/Binding site: carbohydrate (Asn) (covalent) #status
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A;Residues: 1-875 < CDE1>
A;Residues: 1-875 < CDE1>
A;Cross-references: GB:247987; NID:9806378; PIDN:CAA88029.1; PID:9806379
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Reywords: exonuclease; glycoprotein; phosphoprotein; phosphoric diester hydrolase;
C;1-22/Domain: cytosolic *status predicted < CYPM>
F;23-45/Domain: transmembrane *status predicted < TWM>
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A;Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495
A;Reference number: $50428
A;Accession: $50443
                                                                                                                                                                                                                                                                                                                     N;Contains: phosphodiesterase I (EC 3.1.4.1)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 29-Oct-1999
C;Accession: S50443
R;Dietrich, F.S.
   Gaps
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Pred. No. 0.17;
      Indels
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84.6%; Pred. No. 0.0041;
tive 1; Mismatches 1
      Mismatches
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Matches 11; Conservative
      Conservative
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197 YMRAMYPIKTFPN 209
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118 YMIPSFPTQTFPN 130
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-493 <DIE>
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   Matches 11;
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A;Gene: GDB:PDNP1; M6S1; NPPS
A;Gene: GDB:B132615; OMIN:173335
A;Gene: GDB:B226423
A;Gap GDB:B226423
A;Gap position: 6422-6423
C;Superfamily: nucleotide pyrophosphatase; somatomedin B homology
C;Superfamily: nucleotide pyrophosphatase; somatomedin; phosphoric diester hydrolase; tran
E;77-97/Domain: transmembrane #status predicted <TMM>
F;104-144/Domain: somatomedin B homology <SBH1>
F;104-144/Domain: somatomedin B homology <SBH2>
F;145-188/Domain: somatomedin B homology <SBH2>
F;145-188/Domain: somatomedin B homology <SBH2>
F;155-B1hding site: AMP (Thr) (covalent) #status predicted
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A; Residues: 1-905 <VAN

A; Residues: 1-905 <VAN

A; Reference mumber: 1-905 <VAN

A; Reference number: 159055; MUID: 86094275
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A; Residues: 203-219 cRES>

A; Cross-references: GB:M12552; NID:g200234; PIDN:AAA39892.1; PID:g200235

B; Belli, S.I.; van Driel, I.R.; Goding, J.W.

B; Belli, S.I.; van Griel, I.R.; Goding, J.W.

A; Title: Identification and characterization of a soluble form of the plasma cell membra

A; Reference number: S38354; MUID:94039066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasma cell membrane glycoprotein PC-1 - mouse
N.Alternate names: nucleotide pyrophosphatase (EC 3.6.1.9); phosphodiesterase I (EC 3.1.
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Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphoric diester hydrolase; tran
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F:161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:238/Binding site: AMP (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #text_change 05-May-2000
C;Accession: A27410; I59055; S38354
R;van Driel, I.R.; Goding, J.W.
T; Booling, J.W.
T; Booling, J.W.
A;Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from CDNA
A;Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from CDNA
A;Reference number: A27410; MUID:87165906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.8%; Score 69; DB 1; Length 925
100.0%; Pred. No. 0.0009;
Live 0; Mismatches 0; Indels
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Pred. No. 0.0028;
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A; Reference number: S51030; MUID:95094801
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248 MRPVYPTKTFPN 259
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A;Molecule type: DNA
A;Residues: 35-219 <BEL>
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-80 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A27410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I59055
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A; Molecule type: DNA A; Residues: 1-244 <POH>

A; Accession: S19437

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Cyaccession: T09933
R; Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K. submitted to the Protein Sequence Database, June 1999
A; Reference number: 216897
A; Reference number: 216897
A; Residues: 1-461 <-BEV>
A; Residues: 1-461 <-BEV>
A; Cross references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Nap position: 5
A;Introns: 12/3; 37/1; 100/3; 176/2; 272/3; 392/1; 427/1; 479/2; 566/2; 588/3; 677/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Date: 16-011-1999 #sequence_revision 16-Jul-1999 #text_change 15-oct-1999
C'Accession: T09931
FS Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, June 1999
A'Reference number: 216897
A'Recession: T09931
A'Molecule type: DNA
A'Residues: 1-496 < AEV>
A'Residues: 1-496 < AEV>
A'Residues: 1-496 < AEV>
A'Residues: 1-496 orce: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190
C'Genetics: Total Columbia; BAC clone T16L4
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A;Experimental source: clone C27A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C27A7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
     C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
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R;Harris, B.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19132
A;Accession: T19494
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-829 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 2;
Pred. No. 1.1;
1; Mismatches
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Pred. No. 2
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80.0%;
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity
That 8; Conserve
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                                                                                                                                                                                                                                                                                                                    A; Map position: 4
                                                                                                                                                                                                                                                                     C;Genetics:
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Vesst 8, 205-213, 1992
A;Title: The complete sequence of K3B, a 7.9 kb fragment between PGK1 and CRY1 on chrome A;Reference number: $22273; MUID:92245758
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hypothetical protein YCR026c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein YCR247
C;Species: Saccharomyces cerevisiae
C;Date: 31.Mar-1992 #secrevision 31.Mar-1992 #text_change 12-Dec-1997
C;Accession: S19437; S19750; S27380
R;Pohl, F; Richterich, P; Wurst, H.
A;Reference number: S19437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-457 <BEV>
A; Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.200
A; Experimental source: cultivar Columbia; BAC clone T16L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-106,'H',108-119,'F',121-211,'V',213-743 <BOL>
                                                                                                                                                                                                                                                                                                               Riberben, G.; Bolle, P.A.; Gilliquet, V.; Hilger, F. submitted to the Protein Sequence Database, March 1992 A; Reference number: S19433 A; Accession: S19750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 2;
Pred. No. 1.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 2;
Pred. No. 1.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S27380
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 244-743 <BER>
A; Cross-references: EMBL:X59720; MIPS:YCR026c
                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X59720; MIPS:YCR026c R;Berben, G.; Bolle, P.A.; Gilliquet, V.; Hilc
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C,Genetics: A,Map position: 3R C;Keywords: transmembrane protein

65.8%; 61.5%;

Conservative

Query Match Best Local Similarity Matches 8; Conserv

:| | :||:||| 210 FMIPSFPTETFPN 222 1 YMRPVYPTKTFPN 13

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RESULT

64.5%; 80.0%;

Conservative

Local Similarity les 8; Conserv

Query Match Best Local S: Matches 8,

A; Gene: ATSP:T16L4.200 A; Map position: 4

C;Genetics:

A; Molecule type: DNA

94 PVFPTMTFPN 103

1

RESULT F09933

4 PVYPTKTFPN 13

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Gaps

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A;Gene: CESP:C27A7.3
A;Map position: 5
A;Introns: 61/1; 98/3; 191/1; 220/3; 268/3; 340/1; 392/2; 475/2; 496/3; 537/1; 588/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C27A7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19495
R;Harris, B.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219132
A;Reference number: 219495
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-674 <WIL>
A;Cross-references: EMBL:281041; PIDN:CAB02785.1; GSPDB:GN00023; CESP:C27A7.3
                                                                                                                                                                                                                                                                                   unclectide pyrophosphatase homolog - rice
C;Species: Oryza sativa (rice)
C;Species: To C; Tsao, C.V.; Chow, T.; Hsieh, J.; Chen, Z.
Submitted to the EMBL Data Library, April 1995
A;Description: Rice early embryogenesis gene.
A;Reference number: Z14889
A;Reference number: Z14889
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  Score 48; DB 2; Length 496;
Pred. No. 1.8;
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                                                         1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-479 <HSI>
A;Cross-references: EMBL:U25430; NID:g818848; PID:g818849
A;Experimental source: strain Tainung 67
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2;
Pred. No. 2.5;
2; Mismatches
                                                      1; Mismatches
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63.2%;
80.0%;
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Best Local Similarity 70.0%;
Matches 7; Conservative
Query Match 63.2
Best Local Similarity 80.0
Matches 8; Conservative
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146 PVFPTLTFPN 155
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129 PIFPTLTFPN 138
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166 PSFPSKTFPN 175
                                                                                                       4 PVYPTKTFPN 13
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Gaps

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Gaps

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GenCore version 4.5
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OM protein - protein search, using sw model

July 19, 2001, 14:47:09; Search time 16.91 Seconds (without alignments) 26.335 Million cell updates/sec Run on:

US-09-483-831-69\_COPY\_201\_213 Title: Perfect score:

1 YMRPVYPTKTFPN 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P15396 bos taurus	P22413 homo sapien	2 mus π		P25353 saccharomyc	Q02438 hordeum vul	P77989 thermoanaer	P80007 homarus gam	_	'n	P20721 lycopersico	_		Q9mup8 mesostigma		P07184 drosophila	6	P02512 squalus aca	PO4231 mus musculu	PO4230 mus musculu	P01915 mus musculu	P20040 mus musculu	P18468 mus musculu	_	P39465 sulfolobus	P21033 vaccinia vi	P07617 vaccinia vi	P33052 variola vir	_	P48022 lycopersico	_	mus	P55200 mus musculu
SUMMAKIES	DI	PPD1_BOVIN	PC1_HUMAN	PC1_MOUSE	YEB6_YEAST	YCR6_YEAST	E13E_HORVU	BGAL_THEET	CRA2_HOMGA	MD21_HUMAN	MD21_MOUSE	CYSL_LYCES	RRPO_PMV	HMD2_SOLTU	YCF2_MESVI	KIN1_YEAST	CH18_DROME	HMDH_NICSY	CRAB_SQUAC	HB23_MOUSE	HB21_MOUSE	HB22_MOUSE	HB24_MOUSE	HB2I_MOUSE	HB2J_MOUSE	GPT_SULAC	PAP2_VACCC	PAP2_VACCV	PAP2_VARV	SYFA_METJA	HMD2_LYCES	UBA2_YEAST	PGCV_MOUSE	HRX_MOUSE
	DB	-	7	7	Н	ч	Н		Н	П	٦	-	П	٦	7	٦	-	-	-	-	-	٦	٦	-	-	-1	Н	٦	Н	-	-		н,	-
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	Score	69	69	99	54	20	44.5	42	40	40	40	40	40	39	39	39	38	38	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
	Result No.	г	7	m	4	2	9	7	8	6	10	11	12	. 13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	. 28	29	30	31	32	33

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Gaps

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Length 61;

Query Match 90.8%; Score 69; DB 1; Length 61; Best Local Similarity 84.6%; Pred. No. 1.9e-05; Matches 11; Conservative 1; Mismatches 1; Indels

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PC1\_HUMAN STANDARD, PRT; 873 AA.
PC1\_HUMAN STANDARD,
P2411; Q9Y6K3; Q9UP61;
01-AUG-1991 (Rel. 19, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
91\_AMA\_CELL MEMBRANE GIYCOPROTEIN PC-1 [INCLUDES: ALKALINE PHGSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE (EC 3.6.1.9) (NPPASE).
PDNP1 OR PC1 OR NPPS.
PONP1 OR PC1 OR NPPS.
HUMANDA SEQUENCE (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RESULT 2 PC1\_HUMAN ID PC1AH AC P2241: DT 01-AU DT 30-MAN DE PLASM DE PLASM DE EC 3 GN PDNPI OS EUNAN OC EUNAN

34 37 48.7 3969 1 HRX_HUMAN 0003164 homo   35 36.5 48.0 910 1 SCI5_YEAST	Q03164 homo sapien P2224 saccharomyc O28205 archaeoglob P10561 chlamydia t P26257 thermoanaer O04609 homo sapien P35911 cyanidium c P48088 cyanophora P39594 bacillus su P95374 neisseria m P57003 neisseria m			CRC64;
34 37 48.7 33 36.5 48.0 36.5 48.0 36.5 48.0 37 36.5 48.0 37 36.5 47.4 37 36.5 46.1 35.5 46.1 35.5 46.1 35.5 46.1 35.5 46.1 35.5 46.1 35.5 46.1 35.5 46.1 35.5 46.1 35.6 46.1 35.	HRX.F. 1 SC15. 1 SC15. 1 SC15. 1 THIE. 2 S 1 GP/D. 2 S 1 FO/D. 2 S 1 THIE. 2 S 1 THIE. 2 S 1 THIE. 2 S 1 TONB. 3 S	ALIGNMENTS	Created) Last sequence update) Last annotation update) Ca.1.4.1) (5'-EXONUCLEASE) (5'-EXGNET). Cordata; Craniata; Vertebrata; Electiodactyla; Ruminantia; Peconiesterase and identification of ine."; HYDROLYTICALLY REMOVES 5'-NUCL THE 3-'HYDROXY TERMINI OF 3-'HYI	MM;
	36.37 488.7 36.35 488.7 36.47.4 36.47.4 37.5 46.7 35.5 46.7 35.5 46.7 35.5 46.7 35.5 46.7 35.6 46.1 35.7 46.1		PBOVIN PPD136. 01-BOVIN STANI PP1536. 01-APR-1990 (Rel. 14 01-APR-1990 (Rel. 14 01-FB-1994 (Rel. 14 01-FB-1994 (Rel. 14 PHOSPHODIESTERASE I PHOSPHODIESTERASE I BOYDIESTERASE I BOYDIESTERASE I BOYDIESTERASE I BOYDIESTERASE I BOYDIESTERASE I BOYDIESTERASE I FOURT INTERNIE ACTIVI SUCCESSIVELY FRE OLIGO-NUCLECTIPE PIR, A25274; A25274; Hydrolase.	61 AA;

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679
696
121
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P06802;
CARBOHYD
CARBOHYD
                                                     SEQUENCE
                           VARIANT
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 FFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                   -:- CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)O = 2 MONONUCLEOTIDE.
-:- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-:- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROFEIN.
-:- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER OF NON-LYMPHOLD TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE OF THE KIDNEY, CHONDROCYTES, AND EPIDIDYMIS.
-:- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.
                                      MEDLINE=91009202; PubMed=2211644;
Buckley M.F., Loveland K.A., McKinstry W.J., Garson O.M., Goding J.W.;
"Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human
molecule, amino acid sequence, and chromosomal location.";
J. Biol. Chem. 265:17506-17511(1990).
                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
SYRRACELLULAR (POTENTIAL).
SOMATOMEDIN-B LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase;
                                                                                                                                                                                                                                          SEQUENCE OF 93-133 FROM N.A., AND VARIANT GLN-121.
BEDLINE-94048501; Pubmed-10480624;
Pizzutu P. Frittitta I. Argiolas A., Baratta R., Goldfine I.D., Bozzali M., Ercolino T., Scarlato G., Iacoviello L., Vigneri R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                 MEDLINE-92246539; PubMed-1315502;
Funakoshi I., Kato H., Horie K., Yano T., Hori Y., Kobayashi
Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T.,
Yamashina I.;
                                                                                                                                                                                  "Molecular cioning of cDNAs for human fibroblast nucleotide pyrophosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOMATOMEDIN-B LIKE
                                                                                                                                                                                                               Arch. Biochem. Biophys. 295:180-187(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED
N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; pr01663; Phosphodiest; 1.
Pfam; PF01033; Somatcomedin_B; 2.
PRINTS; PR00022; SOWATOMEDINB.
PROSITE; PS00524; SOWATOMEDIN_B; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M57736; AAA63237.1; -.
                                                                                                                                                                                                                                                                                               Tassi V., Trischitta V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001212; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
45
873
92
1136
1127
233
289
691
648
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                           SEQUENCE FROM N.A.
                                                                                                                      SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism
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DOMAIN
DOMAIN
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CARBOHYD
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CARBOHYD
CARBOHYD
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-!- FUNCTION: MAY HAVE A ROLE IN THE REGULATION OF N-GLYCOSYLATION.
-!- CATALYTIC ACTIVITY: HYDROLYTICALLY REMOVES 5'-NUCLEOTIDES
SUCCESSIVELY FROM THE 3'-HYDROXY TERMINI OF 3'-HYDROXY-TERMINATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 169-185 FROM N.A. MEDIINE-86094275; PubMed-3001713; van Driel I.R., Wilks A.F., Pietersz G.A., Goding J.W.; wintine plasma cell membrane antigen PC-1: molecular cloning of cDNA and analysis of expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stearne P.A., van Driel I.R., Grego B., Simpson R.J., Goding J.W.; "The murine plasma cell antigen PC-1: purification and partial amino acid sequence.";
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION, AND SEQUENCE FROM N.A.
MEDLINE=91271356; PubMed=1647027;
Rebbe, N.F., Tong B.D., Finley E.M., Hickman S.;
Identification of nucleotide pyrophosphatase/alkaline
phosphodiesterase I activity associated with the mouse plasma cell
differentiation antigen PC-1.";
Proc. Natl. Acad. Sci. U.S.A. 88:5192-5196(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           van Driel I.R., Goding J.W.; "Plasma cell membrane glycoprotein PC-1. Primary structure deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLIGO-NUCLEOTIDES.
CATALYTIC ACTIVITY: A DINUCLEOTIDE + H(2)0 = 2 MONONUCLEOTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
-:- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
K -> Q.
                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-ANG-1991 (Rel. 19, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PLASMA-CELL MEMBRANE GISCOPROTEIN PC-1 [INCLUDES: ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1); NUCLEOTIDE PYROPHOSPHATASE
                                                                                                                          Score 69; DB 1; Length 873; Pred. No. 0.00031;
                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 2 SOMATOMEDIN-B TYPE DOMAINS.
                                                    /FTId=VAR_008873.
872808C20B048070 CRC64;
                                                                                                                                                                                                                                                                                                                                  871 AA
                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 262:4882-4887(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87165906; PubMed-3104326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE.
MEDLINE=85056299; PubMed=3917281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Immunol. 134:443-448(1985).
                                                                           ¥.
                                                                                                                              90.8%;
100.0%;
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                                                                           99929
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EC 3.6.1.9) (NPPASE)]. PDNP1 OR PC1 OR NPPS.
 679
696
121
                                                                                                                                                                                                                        196 MRPVYPTKTEPN 207
                                                                                                                                                                                                     2 MRPVYPTKTFPN 13
                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus (Mouse)
                                                                         873 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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or send an email to license@isb-sib.ch).
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P25353;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
SOMATOMEDIN-B LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Avalich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Avilles E., Berno A., Brennan T., Carpenter J., Cherry J.M. Chung E., Duncan M., Gurann E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wel Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            Glycoprotein; Transmembrane; Duplication; Signal-anchor; Hydrolase
                                                                                                                                                                                                                                                                                      SOMATOMEDIN-B LIKE.
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 57.4 KDA PROTEIN IN PMP2-VAC8 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 871;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                80848F81071F70AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB 1;
Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                            86.8%; Sco.
91.7%; Pred. No. v..
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                      Pfam; PF01663; Phosphodiest; 1.
Pfam; PF01033; Somatomedin_B; 2.
PRINTS; PR00022; SOMATOMEDINB.
PROSITE; PS00524; SOMATOMEDIN_B; 2.
                                                                              EMBL; J02700; AAA39893.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: TO YEAST YCR26C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
15-JUL-1998 (Rel. 36, Last anno
                                                                                                                                                                                                                                                                                                                                                                                  99487 MW;
                                                                                          EMBL; M12552; AAA39892.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                   PIR; A27410; A27410. MGD; MGI:97370; Pdnp1. InterPro; IPR001212; InterPro; IPR002591;
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841
1136
1127
2833
5333
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196 MRPMYPTKTFPN 207
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                                                                                                                                                                                                                                                                                                                                                                               871 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
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P39997;
                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 244-743 FROM N.A.

SEQUENCE 92245758 PubMed-1574926;

Bolle P.-A., Gilliquet V., Barben G., Dumont J., Hilger F.;

"The complete sequence of K3B, a 7.9 kb fragment between PGKl and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 84.9 KDA PROTEIN IN PMPI-FENZ INTERGENIC REGION
                                                                                                                                                                                              Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 743;
                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pohl F., Richterich P., Wurst H.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                    ll protein.
493 AA; 57354 MW; 10E67A05C6DEDF09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. 2385E9F4BA948B0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
0.47;
                                                                                                                                                                                            Score 54; DB 1;
Pred. No. 0.063;
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO YEAST YEL016C
                      SGD; S0000742; YEL016C.
InterPro; IPR002591; --
Pfam; PF01663; Phosphodiest; 1.
Hypothetical protein.
SEQUENCE 493 AA; 57354 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD; S0000621; YCR026C.
InterPro; IPR002591; -.
Pfam; PF01663; Phosphodiest; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22, Created)
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61.5%;
                                                                                                                                                                                              71.1%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCR026C OR YCR26C OR YCR246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-244 FROM N.A.
EMBL; U18530; AAB64493.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.8
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                             118 YMIPSFPTQTFPN 130
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210 FMIPSFPTETFPN 222
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TRANSMEM 114 135
                                                                                                                                                                                                                                                                                             1 YMRPVYPTKTFPN 13
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                                                                                                                                                                        Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           743 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
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Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum).
Bacteria; Firmicutes; Bacillus/Clostridium group;
Thermoanaerobacter group; Thermoanaerobacter.
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
BETA-GALACTOSIDASE (EC 3.2.1.23) (LACTASE).
LACZ OR LACA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6707;
                                                                                                                              NCBI_TaxID=1757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRA2_HOMGA
P80007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVASION OF GERMINATED BARLEY GRAIN THROUGH ITS ABILITY TO DEGRADE FUNGAL CELL WALL POLYSACCHARIDES.
                                                                                01-0CT-1994 (Rel. 30, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GLUCAN ENDO-1,3-BETA-GLUCOSIDASE GV (EC 3.2.1.39) ((1->3)-BETA-GLUCAN
ENDOHYDROLASE GV) ((1->3)-BETA-GLUCANASE ISOBNZYME GV) (BETA-1,3-ENDOGLUCANASE GV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES IN 1,3-BETA-D-GLUCANS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                        STRAIN-CV. CLIPPER; TISSUE-ROOt, and Leaf;
MEDINE-943043;
XL P., Harvey A.J., Fincher G.B.;
"Heterologous expression of CDNAs_encoding barley (Hordeum vulgare)
                                                                                                                                                                                Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i - FUNCTION: MAY PROVIDE A DEGREE OF PROTECTION AGAINST MICROBIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu P., Wang J., Fincher G.B.;
Frolution and differential expression of the (1-->3)-beta-glucan
endohydrolase-encoding gene family in barley, Hordeum vulgare.";
Gene 120:157-165(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.6%; Score 44.5; DB 1; Length 316; ilarity 81.8%; Pred. No. 1.7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
OCCOAA9D48269B4F CRC64;
                                                        316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. CLIPPER; TISSUE=Root, and Leaf; MEDLINE=93013030; PubMed=1398132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aydrolase; Glycosidase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR000490; -. Pfam; PF00332; Glyco_hydro_17; 1. PROSITE; PS00587; GLYCOSYL_HYDROL_F17; 1.
                                                                                                                                                                                                                                                                                                                                                   (1-->3)-beta-glucanase isoenzyme GV.";
FEBS Lett. 348:206-210(1994).
                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34413 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M96939; AAA21564.1; -. PIR; JC1438; JC1438.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 5-316 FROM N.A.
                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P15737; 1GHS
                                                                                                                                                                                                                                                                           SEQUENCE, FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=4513;
                                                                        Q02438;
01-OCT-1994
01-FEB-1996
                                                        E13E_HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
ACT_SITE
SEQUENCE
                         RESULT 6
E13E_HORVU
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Eur. J. Biochem. 19:1407-417(1991).
-!- FUNCTION: BINDS THE CAROTENIOL ASTAXANTHIN WHICH PROVIDES THE BLUE.
-: COLORATION TO THE CARAPACE OF THE LOBSTER.
-: SUBUNIT: OLIGOMER; CAN FORM DIMERS (BETA-CRUSTACYANIN); OR
COMPLEXES OF 16 SUBUNITS (ALPHA-CRUSTACYANIN). THERE ARE FIVE
TYPES OF SUBUNITS: Al, A2, A3, C1 AND C2.
-: SUBCELLULAR LOCATION: EXTRACELLULAR, CARAPACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                    -- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
-- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete sequence and model for the A2 subunit of the carotenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUNAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
01-OCT-1994 (Rel. 30, Last annotation update)
EURSTRACTANIN A2 SUBBUNIT.
HOMATUS gammarus (European lobster) (Homarus vulgaris).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eucarida; Decapoda; Pleocyemata; Astacidea;
Mephropoldea; Nephropidae; Homarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.3%; Score 42; DB 1; Length 743; 53.8%; Pred. No. 11; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOPHILE (BY SIMILARITY). FE011FF517E51DFC CRC64;
                                          Zverlov V.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keen J.N., Caceres I., Eliopoulos E.E., Zagalsky P.F., Findlay J.B.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001649; --
Pfam; PF00703; Glycc_hydro_2; 1.
PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91224133; PubMed=2026162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 743 AA; 85796 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y08557; CAA69850.1; -.
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
SEQUENCE FROM N.A.
STRAIN-ATCC 33223 / 39E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Glycosidase.
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454 YMGHMYPTKSYDN 466
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743 AA

STANDARD;

BGAL\_THEET P77989;

BGAL\_THEET RESULT e S

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MIM; 601467;
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MD21_MOUSE
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  δλ
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"Evidence for an interaction of the metalloprotease-disintegrin tumour necrosis factor alpha convertase (TACE) with mitotic arrest deficient 2 (MAD2), and of the metalloprotease-disintegrin MDC9 with a novel
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98301442; PubMed-9637688;
Fang G., Yu H., Kirschner M.W.;
"The checkpoint protein MAD2 and the mitotic regulator CDC20 form
ternary complex with the anaphase-promoting complex to control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1)
                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li Y., Benezra R.; "Identification of a human mitotic checkpoint gene: hsMAD2."; Science 274:246-248(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20165182; PubMed-10700282;
Luo X., Fang G., Coldiron M., Lin Y., Yu H., Kirschner M.W.,
                                                                                                                                                                                                                                                                                                        DB 1; Length 174; 5.2;
                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jin D.-Y., Jeang K.-T.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                               AC47FAA650C5E44E CRC64;
-! - SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 AA.
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
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Biochem. J. 343:673-680(1999).
                                                                                            Pfan, PF00061; lipocalin; 1.
PRINTS; PR00179; LIPOCALIN.
PRINTS; PR01273; INVPERTCOLOR.
PROSITE; PS00213; LIPOCALIN; 1.
Proment; Lipocalin; Transport.
DISULFID 12 119 BY S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes Dev. 12:1871-1883(1998).
                                                                                                                                                                                                                                           SEQUENCE 174 AA; 19670 MW;
                                                                                                                                                                                                                                                                                                        52.6%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF 11-195
                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 87.5
Matches 7; Conservative
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INTERACTION WITH ADAM17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                     InterPro; IPR000566; -. InterPro; IPR002345; -.
                                                                               IPR003057; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH CDC20.
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                                                                                                                                                                                                                                                                                                                                                                                       5 VYPTKTFP 12
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80 VYPTKEFP 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAD2L1 OR MAD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MD21_HUMAN
Q13257;
                                                                               InterPro;
                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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"Structure of the Mad2 spindle assembly checkpoint protein and its interaction with Cdc20.";
Nat. Struct. Biol. 7:224-229(2000).

i.e. FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ACTIVITY OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pubbles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
Dobles M., Liberal V., Scott M.L., Benezra R., Sorger P.K.;
"Chromosome missegregation and apoptosis in mice lacking the mitotic checkpoint protein Mad2.";
Cell 101:635-645(2000).
-!- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT WHICH MONITORS THE PROCESS OF KINETOCHORE-SPINDLE ATTACHMENT AND DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0921B5; 09J153;
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
MITOTIC SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2A (MAD2-LIKE 1).
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STRAIN-C57BL/6J; TISSUE-Embryo;
Jin D.-Y., Jeang K.-T.;
"Identification of a novel component of the spindle assembly checkpoint in mammalian cells.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 205;
                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: INTERACTS WITH CDC20 AND WITH ADAM17 (TACE).
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003511; -.
Pfam; PF02301; HORMA, I.
Cell cycle; Mitosis; Nuclear protein; 3D-structure.
SEQUENCE 205 AA; 23510 MW; B8DCBF0043836764 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1;
Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AA.
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54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U65410; AAC50781.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U31278; AAC52060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-00.
                                                                                                                                                                                                                                                                                            METAPHASE PLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YMRPVYPTKTF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 YORGIYPSETF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
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InterPro; IPR000169; -. InterPro; IPR000668; -.
                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
10-NOV-1995 (Rel. 32, Last annotation update)
10-W-TEMPERATURE-INDUCED CYSTEINE PROTEINASE PRECURSOR (EC 3.4.22.-)
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CV. VFNT CHERRY;
SChaffer M.A., Fischer R.L.;
"Analysis of mRNAs that accumulate in response to low temperature identifies a thiolprotease in tomato.";
Plant Physiol. 87:431-436(1988).
-!- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE PAPAIN FAMILY OF THIOL PROTEASES.
   INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T -> A (IN REF. 1).
C -> S (IN REF. 1).
T -> I (IN REF. 1).
; A9F3F28BC4C9738E CRC64;
                                      SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE A METAPHASE PLATE (BY SIMILARITY).
-!- SUBULT: INTERACTS WITH CDC20.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 1
Pred. No. 6.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 AA
                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE MAD2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF261919; AAF69525.1; -. InterPro; IPR003511; -. Pfam; PF02301; HORMA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23598 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U83902; AAD09238.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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; P00785; ZACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell cycle; Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | :||::||
33 YQRGIYPSETF 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 AA;
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Best Local Similarity
Matches 6; Conserv
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MEROPS; C01.029; -. InterPro; IPR000118;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pfam; PF01443; Viral_helicase1; 1.
ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA REPLICATION PROTEIN (176 KDA PROTEIN) (ORF 1) [CONTAINS: RNA-
DIRECTED RNA POLYMERASE (EC 2.7.7.48); PROBABLE HELICASE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papaya mosaic potexvirus (PMV)
Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
NCBL_TaxID=12181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Gen. Virol. 70:2325-2331(1989).
-!- FUNCTION: RNA-REPLICATION. THE CENTRAL PART OF THIS PROTEIN POSSIBLY FUNCTIONS AS A ATP-BINDING HELICASE.
                                                                                                                                                                                                                                                                                                                                                               LINKED (GLCNAC. . .) (POTENTIAL) D42AC73944010928 CRC64;
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                                                                                                                                                        ACTIVATION PEPTIDE (POTENTIAL).
LOW-TEMPERATURE-INDUCED CYSTEINE
PROTEINASE.
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52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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176320 MW; 6CA4282C6A082622 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of papaya mosaic virus RNA.";
J. Gen. Virol. 70:2325-2331(1989).
                                                                                                                 Hydrolase; Thiol protease; Zymogen; Glycoprotein.

NON TER 1 1 ACTIVATION PEPTIDE (1)

PROPEP <1 17
Pfam: PF00112; Peptidase_C1; 1.
Pfam: PF00196; granulin: 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                             BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sit T.L., Abouhaidar M.G., Holy S.;
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MEDLINE-89381685; Pubmed-2778435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                          37429 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.6%;
58.3%;
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Best Local Similarity 58.3.
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1547 AA;
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE
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P20951;
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DISULFID
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SEQUENCE
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YCF2_MESVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEPALS AND OVARIES.
                                                                                                                                                                                                  Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Solanum.
                                                                                                                                    01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (EC 1.1.1.34) (HMG-
                                                                                                                                                                                                                                                                                         STRAIN-CV. KENNEBEC; TISSUE-Tuber; MEDLINE-97201488; PubMed-9049274; Korth K.L., Stermer B.A., Bhattacharyya M.K., Dixon R.A.; Hardracharyya M.K., Dixon R.A.; HMG-COA reductase gene families that differentially accumulate transcripts in potato tubers are developmentally expressed in floral
                                                                                                                                                                                                                                                                                                                                                                  Plant MOI. Biol. 33:545-551(1997).

-!- FUNCTION: CATALXZES THE SYNTHESIS OF MEVALONATE. THE SPECIFIC PRECURSOR OF ALL ISOPRENDID COMPOUNDS PRESENT IN PLANTS.
-!- CATALYTIC ACTIVITY: (F) MEVALONATE + COA + 2 NADP(+) = (S)-3-HYDROXX-3-METHYLGIUTARYL-COA + 2 NADPH.
-!- PATHWAY: MEVALONATE BIOSYNTHESIS, PLANT ISOPRENOID BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pran; PR0368; HWG-CoA_red; 1.
PRINTS; PR00071; HWGCOARDTASE.
PR05TTE; PS00066; HMG_COA_REDUCTASE_1; 1.
PR05TTE; PS00318; HMG_COA_REDUCTASE_2; 1.
PR05TTE; PS01192; HMG_COA_REDUCTASE_3; 1.
PR05TTE; PS50065; HMG_COA_REDUCTASE_4; 1.
Oxidoreductase; Glycoprotein; Endoplasmic_reticulum; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- TISSUE SPECIFICITY: EXPRESSED IN YOUNG FLOWERS AND IN MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoprene biosynthesis; NADP; Multigene family.
DOMAIN 1 112 MEMBRANE-BOUND (BY SIMILARITY).
DOMAIN 113 183 LINKER (BY SIMILARITY).
DOMAIN 184 595 CATALYTIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL BASE (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENT
                                                                                                 595 A.A.
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Mendel; 10574; Soltu;1091;10574.
                                                                                                                        01-OCT-2000 (Rel. 40, Created)
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                        YPTKTFDN 416
          6 YPTKTFPN 13
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SEQUENCE 890 AA; 103935 MW; 43CAEEE991AF2C4B CRC64;
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Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Mesostigmataceae; Mesostigma.
NCBI_TaxID=41882;
OFA7069849D41D57 CRC64;
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ed. No. 43;
Mismatches 3
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01-0cT-2000 (Rel. 40, Last sequence update)
01-0cT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 103.9 KDA PROTEIN YCF2 (RF2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       branch of green plant evolution.";
Nature 403:649-652(2000).
-!- SIMILARITY: BELONGS THE YCF2 FAMILY.
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MEDLINE-20150907; PubMed=10688199;
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` hes 6; Conserv
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595 AA;
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C Saccharomycetales; Saccharomycetaceae; Saccharomyces.

W NEAL TaxID-493;

R H T "You yeast genes that encode unusual protein kinases.";

R H MINING. S. JASHON N.A.

R MAIN-1958; PubMed-205/560;

RA MAIN-1959; PubMed
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Db 802 YMRPPMPSSAYP 813

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Gaps

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Score 39; DB Pred. No. 52; 2; Mismatches

51.3%; 50.0%;

Query Match Best Local Similarity

Conservative

Matches

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DB 1; Length 1064; 52; hes 4; Indels

Search completed: July 19, 2001, 14:47:09 Job time: 171 sec

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July 19, 2001, 14:46:48; Search time 42.51 Seconds (without alignments) 40.460 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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sp\_unclassified:\* sp\_vertebrate:\*

sp\_virus:\*

sp\_rodent:\* sp\_plant:\*

Q9rle6 mus musculu Q13822 homo sapien Q15117 homo sapien Q13827 homo sapien Q64610 rattus norv Q88827 rattus norv 063490 rattus norv P97676 rattus norv 090761 fowlpox vir 0915h1 fowlpox vir 0915h1 fowlpox vir 09181 arabidopsis 098u81 arabidopsis P90754 ceenorhabdi Q9npz3 homo sapien Q9p1p6 homo sapien P97675 rattus norv P70641 rattus norv 014638 homo sapien Description SUMMARIES Q9R1E6 Q13822 Q15117 Q13827 964610 98827 99822 99822 99826 97675 97641 01638 063490 99767 99776 99776 99776 Query Match Length DB .00 8 Score Result Š

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BUDLINE-96158950; PubMed-8579579;

Lee H.Y., Murata J., Clair T., Polymeropoulos M.H., Torres R.,

Manrow R.E., Liotta L.A., Stracke M.L.;

"Cloning, chromosomal localization, and tissue expression of autotaxin
from human teratocarcinoma cells.";

Biochem. Biophys. Res. Commun. 218:714-719(1996).

EMBL; L46720; AAB00855.1;

InterPro; IPR001604;

InterPro; IPR001604;

InterPro; IPR001604;
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"Molecular cloning and chromosomal assignment of the human brain-type phosphodiesterase I/nucleotide pyrophosphatase gene (PDNP2).";
Genomics 30:380-384(1995).
EMBL: D45421: BAA0820.1; -.
InterPro; IPR001212; -.
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Kawagoe H., Soma O., Goji J., Nishimura N., Narita M., Inazawa J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00524; SOMATOMEDIN_B; 2.
            PRT;
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MEDLINE=95074054; PubMed=7982964;
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Matches 13; Conservative
            PRELIMINARY;
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL: Li35544; AAA6475-1; -.

InterPro; IPR001212; -.
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SEQUENCE 915 AA; 105246 MW; 2BE6135CCD837780 CRC64;
InterPro; IPR001604; -.
InterPro; IPR002591; -.
Pfam; PF0103; Somatomedin_B; 2.
Pfam; PF01053; SomatoMeblin_B; 2.
PRINTS; PR00022; SOMATOMEDIN_B.
PROSITE; PS000524; SOMATOMEDIN_B; 2.
SMART; SMO477; NUC; 1.
SEQUENCE 863 AA; 99040 MW; 318EA2BBICEA7A55 CRC64;
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PROSITE; PS00524; SOMATOMEDIN_B; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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01-NOV-1996 (TrEMBLrel. 01, Create
01-NOV-1996 (TrEMBLrel. 01, Last s
01-MAR-2001 (TrEMBLrel. 16, Last a
PHOSPHODIESTERASE I (EC 3.1.4.1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01033; Somatomedin_B; 2. Pfam; PF01663; Phosphodiest; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OKT-2001 (TrEMBLrel. 16, Last annotation update)
DJ131F15.2 (PROSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHARSE :
(HOMOLOGGUS TO MOUSE LY-41 ANTIGEN) (PC1, NPPS)) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.8%; Score 69; DB 4; Length 845; 100.0%; Pred. No. 0.00092; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                Peck A.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL117378; CAB99365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bozzall M., Pizzuti A., Trischitta E.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF110304; AAF36094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 845 AA; 96844 MW; C2DD58248BDAC52E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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PROSITE; PS00524; SOMATOMEDIN_B;
SMART; SM00477; NUC; 1.
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001212; -.
InterPro; IPR001604; -.
InterPro; IPR001504; -.
InterPro; IPR001501; -.
Pfam; PF01033; Somatomedin_B; 2.
Pfam; PF01063; Phosphodiest; 1.
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Best Local Similarity 100.
Matches 12; Conservative
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AF110288;
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Q9P1P6;
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EMBL;
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Q9P1P6
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                                                                   STRAIN-SPRAGUE-DAWLEY, TISSUE-BRAIN;
MEDLINE-55050605; PubMed-7961762;
Narita M., Goji J., Nakamura H., Sano K.;
"Molecular cloning, expression, and localization of a brain-specific phosphodiesterase I/nucleotide pyrophosphatase (PD-I alpha) from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A SAAOda H., Asano T., Ogihara T.;

N terminal of the plasma cell membrane glycoprotein PC-1.";

Submitted (SEP-1998) to the FMBL/GenBank/DDBJ databases.

R EMBL; AB017596; BAA33393.1;

R InterPro: PRO0022; SOMATOMEDINB.

R PRINTS; PRO0022; SOMATOMEDINB.

R PROSITE; PRO024; SOMATOMEDINB.

R PROSITE; PRO024; SOMATOMEDINB.

R SMART; SM00201; SO;

T NON TER 257 257

SEQUENCE 257 AA; 28306 MW; CF348E474FBDAFED CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PLASMA CELL MEMBRANE GLYCOPROTEIN (FRAGMENT).
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                                                                                                                                                                                         braff.;
J. Biol. Chem. 269:28235-28242(1994).
EMBL; D28560; BRA05910.1; -.
InterPro; IPR001213; -.
InterPro; IPR001504; -.
InterPro; IPR002591; -.
Pfam: PF01033; Somatomedin_B; 2.
Pfam: PF01663; Phosphodiest; 1.
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PROSITE; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00477; NUC; 1.
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
                                                  SEQUENCE FROM N.A.
     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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09NPZ3;
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                                                                                                                                           Sano K.;
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014638;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ALKALINE PHOSPHODIESTERASE.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Blochemical and molecular identification of distinct forms of alkaline phosphodiesterase I expressed on the apical and basolateral plasma membrane surfaces of rat hepatocytes.";
Hepatology 25:995-1002(1997).
EMBL; U78787; PR0011951; -.
InterPro; IPR001212; -.
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STRAIN-SPRAGUE-DAWLEY;
MEDLINE-97250927; PubMed-9096610;
Scott L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.
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                                                                                                                                                                                                                                                                              Length 925;
                                                                                                                                                                                                                                                            Score 69; DB 4; Length 922; Pred, No. 0.001;
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                                                                                                                                                         PRINTS; PR00022; SOMATOMEDINB.
PROSTITS; PS00524; SOMATOMEDIN_B; 2.
SMART; SM00477; NUC; 1.
SEQUENCE 925 Aa. 104924 MW; OECAA063801CAFEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99166 MW; 8FEB9A482173D377 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                875 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
                                                                                                                                                                                                                                                                                        100.08; Preα. ...
+ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
EMBL; AF110301; AAF36094.1; JOINED.
EMBL; AF110302; AAF36094.1; JOINED.
EMBL; AF110303; AAF36094.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002591; -.
Pfam; PF01033; Somatomedin_B; 2.
Pfam; PF01663; Phosphodiest; 1.
                                                                              InterPro; IPR001604; -.
InterPro; IPR002591; -.
Pfam; PF01033; Somatcomedin_B; 2.
Pfam; PF01663; Phosphodiest; 1.
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                                                                                                                                                                                                                                                                              90.88;
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                                                                                                                                                                                                                                                                              Query Match 90.8
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                            InterPro; IPR001212;
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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SEQUENCE
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P97675
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MEDLINE=98008933; PubMed=9344668;
Piao J.-H., Goding J.W., Nakamura H., Sano K.;
Molecular cloning and chromosomal localization of PD-Ibeta (PDNP3), a new member of the human phosphodiesterase I genes.";
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE BETA (EC 3.1.4.1)
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                                                                                                                                                                                                                           "Molecular cloning of phosphodiesterase I cDNA from rat small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 11; Length 876; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-SMALL INTESTINE, PROXIMAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF005632; AAC51813.1; -.
EMBL; AC005587; AAD05192.1; -.
                                                                                                                                                                                                                                                                                    Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; D30649; BAA06333.1; -.
InterPro; IPR001212; -.
InterPro; IPR001504; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hou S., Wohldmann P., Le T.; "The sequence of Homo sapiens PAC clone DJ0988G15."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D2F772C34A0C437A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  875 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002591; -- Pfam; PF01033; Somatomedin_B; 2. Pfam; PF01663; Phosphodiest; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99328 MW;
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SEQUENCE OF 189-875 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.5%;
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00477; NUC; SEQUENCE 876 AA; 9
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                                                                                 NCBI_TaxID=10116;
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MEDLINE-97250927; Pubmed-9096610;
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 SEQUENCE FROM N.A.
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                                  Maurice M.;
                                                                                                                                                                                                   Query Match
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090761
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                       Deissler H., Lottspeich F., Rajewsky M.F.; "Affinity purification and cDNA cloning of rat neural differentiation and tumor cell surface antigen gpl30RB13-6 reveals relationship to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NGBI_TaxID=10116;
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                                                                                                           Length 875;
                                                                                                                                1; Indels
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                                                                           875 AA; 100096 MW; 329CF41667497BC4 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                           Score 65; DB 4;
Pred. No. 0.0048;
L; Mismatches
                                                                                                                                                                                                                                   875 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfan; PF01033; Somatomedin_B; 2.
Pfam; PF01663; Phosphodiest; 1.
PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
                   Pfan; PF01033; Somatomedin_B; 2.
Pfan; PF01663; Phosphodiest; 1.
PROSITE; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                      human and murine PC-1.";
J. Biol. Chem. 270:9849-9855(1995).
EMBL; Z47987; CAA88029.1; -.
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                                                                                                           85.5%;
84.6%;
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                                                                                                       Query Match 85.5
Best Local Similarity 84.6
Matches 11, Conservative
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                                                                                                                                                                                                                                 PRELIMINARY;
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InterPro; IPR001604; -. InterPro; IPR002591; -.
                                                     SMART; SM00477; NUC; 1. Hydrolase.
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196 YMRAMYPTKTFPN 208
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197 YMRAMYPTKTFPN 209
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SMART; SM(
           InterPro;
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P97676
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"The major acidic fibroblast growth factor (aFGF)-stimulated
phosphoprotein from bovine liver plasma membranes has aFGF-stimulated
kinase, autcadenylylation, and alkaline nucleotide phosphodiesterase
activities.";
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                                             "Biochemical and molecular identification of distinct forms of alkaline phosphodiesterase I expressed on the apical and basolateral plasma membrane surfaces of rat hepatocytes."; Hepatology 25:995-1002(1997).
EMBL; U78788; AAB61336.1; -.
InterPro; IPR001212; -.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
260 KDA MAJOR ACIDIC FIBROBLAST GROWTH FACTOR-STIMULATED
PHOSPHOPROTEIN (FRAGMENT).
PHOSPHOPROTEIN (FRAGMENT).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
L.J., Delautier D., Meerson N.R., Trugnan G., Goding J.W.,
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ALKALINE PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.5%; Score 65; DB 11; Length 875; 84.6%; Pred. No. 0.0048;
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91.7%; Pred. No. 0.0002;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                      99071 MW; 4205F263E8A933EA CRC64;
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SEQUENCE 32 AA; 3699 MW; 5CCFFA9EB55E6927 CRC64;
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Pfam; PF01663; Phosphodiest; 1.
PR0517E; PS00524; SOMATOMEDIN_B; UNKNOWN_2.
SWART; SM00201; SO; 1, 99071 MW; 4205F263ERA9
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M. MEDLINE=98325194; Pubbled=9658122;
Laidlaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.;
Indidaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.;
Toron T. 
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Avipoxvirus.
NCBI_TaxID=10261;
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Gaps

Search completed: July 19, 2001, 14:46:49 Job time: 172 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF; \*\_melanoma cell; tumour; antibody; cancer diagnosis; therapy. (USSH ) US DEPT HEALTH & HUMAN SERVICES. AAR86596 standard; Protein; 915 AA. 95WO-US06613 94US-0346455. 94US-0249182. (first entry) A2058 autotaxin protein.

Autotaxin motility stimulating protein, and DNA encoding it - used in cancer diagnosis and therapy

Murata J, Schiffmann E, Stracke M;

Claim 4; Page 91-94; 112pp; English

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           AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This sequence represents the full length protein sequence of the A2058 melanoma cell line ATX protein. ATX is an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. The tumourcus form of ATX is a secreted protein, while the transmembrane bound form is not present in tumour cells. The DANA encoding this sequence can be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXX, while having little effect on the membrane form of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Autotaxin phosphodiesterase catalytic site"
                                                                                                                                                                                                                                                                                                                                                                                             Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; horrapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodissterase activity; ATP pyrophosphatase activity; ATP prophosphatase activity; ATP prophosphatase activity; melanoma.
                                                             LSVSSFILPHRPDNEESCNSSEDESKWVEELMKMHTARVRDIEHLTSLDFFRKTSRSYPE
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obesity, stimulate glucose uptake by cells and inhibit lipolysis
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                                                                                                                                            KGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA 240
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                                           Length 915;
Transgenic animals that overexpress autotaxin are models for
                                                           Indels
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Best Local Similarity 100.
Matches 915; Conservative
       human metabolic diseases.
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New autotaxin proteins, useful e.g. for treating diabetes mellitus and
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Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (MIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).

Transgenic animals that overexpress autotaxin are models for
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                                                                                                                                                                                                                                       Human; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity;
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                                                                                                                                                                                                                                                                                                                                                                                                 ATPase, adenosine-5'-triphosphatase activity; teratocarcinoma
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/label= RGD_binding_domain
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                                                                                                                                                                                  Human teratocarcinoma autotaxin.
AAY71988 standard; Protein;
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Best Local Similarity 93.8%;
Matches 858; Conservative
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/note= "A
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adipocyte, hypoglycemic, antidiabetic, anorectic, antilipemic,
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         TFHLRGREKFNHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTILRWLTLPDHER
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GRCFELQEAGPPDCRCDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHC
                                     SEDCLARGDCCTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMK
                                                                          KGSKVMPNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDA
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The present sequence is human autotaxin protein.

Autotaxin is a glycoprotein cytokine which increases
insulin signalling in adipose tissue by producing substrate for
adenosine receptors, resulting in inhibition of lipolysis,
decreased hepatic gluconeogenesis and serum glucose levels, and
increased insulin sensitivity. It also inhibits differentiation
of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'.
Itriphosphatase (ATPase) and ATP pyrophosphatase activities.
Autotaxin and its analogues are used to stimulate glucose uptake
trathent of non-insulin dependent diabetes (NIDDM) in humans,
or generally any condition associated with elevated serum levels
of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia).
Transgenic animals that overexpress autotaxin are models for
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
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therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity.
                                                                                                                                               44..45
123..125
7.label= RGD_binding_domain
197..209
7.note= "Putative phosphodiesterase active site"
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/note= "Putative transmembrane domain"
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3; Mismatches
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Pred. No. 0;
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                                                                                                       Location/Qualifiers
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93.7%;
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Matches 848; Conservative
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            NHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTILRWLTLPDHERPSVYAFYSEQ
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AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. The tumourcus form of ATX is a secreted protein, while the transmembrane bound form is not present in tumour cells. The cDNA encoding this sequence can be used in a vector, to transform cells. recombinant cells can then be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXT, while having little effect on the membrane form of AXT.
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                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
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446 420 300 506 626 CHDFDELCLKTARGWECTKDRCGEVRNEENACHCSEDCLARGDCCTNYQVVCKGESHWVD IVGQLMDGLKQLKLRRCVNVIFVGDHGMEDVTCDRTEFLSNYLTNVDDITLVPGTLGRIR DLLGLKPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFDLGCTCDDKVE DDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIEKLRSCGTHSPYMRPVY SKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANNRRIEDIHLLVERRWHV **ARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYKTKVPPFENIELYNVMC** PTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKFNHRWGGQPLWITATK SYGSPFTPAKRPKRKVAPKRRQERPVAPPKKRRRKIHRMDHYAAETRQDKMTNPLREIDK ö Length 829; Indels 17; DB Score 4533; DI Pred. No. 0; 0; Mismatches ö 90.3%; Conservative Best Local Similarity Matches 828; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
                                                                                                                                                                                                                                                                                                                                               adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes melitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATP parcohosphatase activity; ATP parcohosphatase activity; ATP parcohosphatase activity; ATP parcohosphatase activity; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is variant (5236T) of rat autotaxin protein. Autotaxin is a glycoprotein cytokine which increases insulin signaling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NTDNM) in humans.
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                                                                                pknkldelnkrlhtkgsteerhllygrpavlyrtrydilyhtdfesgyseiflmllwtsy
                                                                   DAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPIFDYDYDGLHDTEDKIK
                                                                                                                QYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPHRPDNEESCNSSEDESK
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                      TVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCLAYKNDKQMSYGFLFPPYLSSSPEAKY
                                   autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
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with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.

Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in page 101-104 of sequence listing (AAY71986).
                                                                                                                                                                                                                                                       11 QIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCKGRCFELQEAG
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                                                                                                                                                                                  Score 4430.5;
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30; Mismatches
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Matches 803
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adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATP parcohosphatase activity; ATP activity; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autotaxin is adjunced that it is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic glucomeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine 5'-triphosphatase (ATPASS) and ATP pyrophosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipideamia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is variant ($289T) of rat autotaxin protein.
                                                                                                                                                                                                                                                                   Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
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289
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131 CTNYQVVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGFRASYMKKGSKVMPNIE 190
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11 QIISLFTFAVGVSICLGFTAHRIKRAEGWEEGPPTVLSDSPWTNISGSCKGRCFELQEAG 70
          KLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKF
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DB 22; 19;

88.3%; Score 4430.5; 88.7%; Pred. No. 0; ive 30; Mismatches

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Autotaxin is a glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.

Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphatese activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent clabetes (MIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress outcaxin are models for human metabolic diseases.

Note: The present sequence is not shown in the specification but is derived from rat autotaxin protein sequence found in
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                                                  adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATP activity; ATP activity; mutant; mutein; variant.
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                                        autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          page 101-104 of sequence listing (AAY71986).
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88.7%; Pred. No. 0;
ive 30; Mismatches
                                                                                                                                                                Location/Qualifiers
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               variant (R265K)
                                                                                                                                                                                                                                                                 05-MAY-2000; 2000WO-US12402.
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Matches 803; Conservative
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               Rat autotaxin
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                          FDYDYDGLHDTEDKIKQYVEGSSIPVPTHYYSIITSCLDFTQPADKCDGPLSVSSFILPH
NHRWWGGQPLWITATKQGVKAGTFFWSVVIPHERRILTILRWLTLPDHERPSVYAFYSEQ
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Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDW; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; mutant; mutein; variant.
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246 nhrwwggqplwitatkggvragtffwsvsipherriltildylslpdnerpsvyafyseq
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                                                                                                                                                                   196..208
//note= "Autotaxin phosphodiesterase catalytic site"
585..595
/label- Epitope
/note= "This region is specifically claimed in claim 10"
                                            143..158
//label Epitope
//note= This region is specifically claimed in claim 10"
                                                                                                            /label- Epitope
/note= "This region is specifically claimed in claim 10;
This region is absent in rat brain autotaxin designated
as PD-Ialpha sequence (AAY71989)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein cytokine which increases insulin signalling in adipose tissue by producing substrate for adenosine signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased heptic glucomeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes. Autotaxin has type I phosphodiesterase, adenosine 5'-triphosphatase (Arpass) and Arp pyrophosphates activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53;
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                "Putative transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 4426.5;
Pred. No. 0;
31; Mismatches
                                         RGD_binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 101-104; 126pp; English
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/label- R
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Matches 802; Conserv
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                           Binding-site
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Rat; autotaxin; lipolysis; gluconeogenesis; insulin sensitivity; adipocyte; hypoglycemic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; mutant; muteni; variant.
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                                                                                                     RRIEDIHLLVERRWHVARKPLDVYKKPSGKCFFQGDHGFDNKVNSMQTVFVGYGPTFKYK
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                                                    NVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANN
                                                                                                                                                                                     GFLFPPYLSSSPEAKYDAFLVTNMVPMYPAFKRVWNYFQRVLVKKYASERNGVNVISGPI
                                                                                                                                                                       TKVPPFENIELYNVMCDLLGLKPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY71995 standard; Protein;
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Synthetic.
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Autotaxin is a glycoprotein cytokine which increases insulin
signalling in adipose tissue by producing substrate for adenosine
receptors, resulting in inhibition of lipolysis, decreased hepatic
gluconeogenesis and serum glucose levels, and increased insulin
sensitivity. It also inhibits differentiation of adipocytes.

Autotaxin has type I phosphodissterase, adenosine-5'-triphosphatase
(ATPase) and ATP pyrophosphatase activities. Autotaxin and its
analogues are used to stimulate glucose uptake by cells, particularly
to reduce serum glucose levels for treatment of non-insulin dependent
clabetes (NIDDM) in humans, or generally any condition associated
with elevated serum levels of glucose, lipid or free fatty acid
(e.g. obesity or dyslipidemia). Transgenic animals that overexpress
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                 /note= "Wild type Ala substituted by Val"
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88.6%; Pred. No. 0;
ive 30; Mismatches
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                                                                                                                   05-MAY-2000; 2000WO-US12402.
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Best Local Similarity 88.6
Matches 802; Conservative
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Misc-difference 194
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Autotaxin has type I phosphodiesterase, adenosine-5'-triphosphatase (ATPase) and ATP pyrophosphates activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHYANN 490
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                                                New autotaxin proteins, useful e.g. for treating diabetes mellitus obesity, stimulate glucose uptake by cells and inhibit lipolysis -
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                                                                                                               present sequence is variant (A93V) of rat autotaxin protein.
                                                                                                                                                                                                                                                                                                                                                                                   Length 858;
                                                                                                                                                                                                                                                                                         Note: The present sequence is not shown in the specification
                                                                                                                                                                                                                                                                                                         derived from rat autotaxin protein sequence found in
                                                                                                                                                                                                                                                                                                                                                                                                          20; Indels
                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                     page 101-104 of sequence listing (AAY71986).
                                                                                                                                                                                                                                                                                                                                                                                 88.1%; Score 4422.5;
88.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                          31; Mismatches
                                                                                      Disclosure; Page -; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity ....
Matches 801; Conservative
                        WPI; 2001-007397/01
                                                                                                                                                                                                                                                                                                                                              Sequence
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AAR86559-R86596 represent autotaxin (ATX) and fragments of it. This sequence represents the full length protein sequence of the teratocarchinoma N-tera 2D1 ATX protein. ATX is an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. The tumourous form of ATX is a secreted protein, while the transmembrane bound form is not present in tumour cells. The cDNA encoding this sequence can be used in a vector, to transform cells. The recombinant cells can then be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF; melanoma cell; tumour; antibody; cancer diagnosis; therapy.
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sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXT, while having little effect on the membrane form of AXT.
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                                                          Length 849;
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                                                           86.5%; Score 4341; DB 17;
87.9%; Pred. No. 0;
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This sequence is designated as nucleotide pyrophosphatase.
This sequence is designated as nucleotide pyrophosphatase.

(PD-lalpha), Autotaxin is a glycoprotein cytokine increases insulin signalling in adipose tissue by producing substrate for adenosine receptors, resulting in inhibition of lipolysis, decreased hepatic gluconeogenesis and serum glucose levels, and increased insulin sensitivity. It also inhibits differentiation of adipocytes.

Autotaxin has type I phosphatase activities. Autotaxin and its analogues are used to stimulate glucose uptake by cells, particularly to reduce serum glucose levels for treatment of non-insulin dependent diabetes (NIDDM) in humans, or generally any condition associated with elevated serum levels of glucose, lipid or free fatty acid (e.g. obesity or dyslipidemia). Transgenic animals that overexpress autotaxin are models for human metabolic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New autotaxin proteins, useful e.g. for treating diabetes mellitus and obesity, stimulate glucose uptake by cells and inhibit lipolysis -
                                                                                                                                                                                                                                                                                                     adipocyte; hypoglycenic; antidiabetic; anorectic; antilipemic; therapy; metabolic disease; obesity; dyslipidemia; serum glucose; non-insulin dependent diabetes mellitus; NIDDM; transgenic animal; type I phosphodiesterase activity; ATP pyrophosphatase activity; ATPase; adenosine-5'-triphosphatase activity; pp-Ialpha; brain; nucleotide pyrophosphatase.
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                                                                                                                                                                                                                                                                        autotaxin; lipolysis; gluconeogenesis; insulin sensitivity;
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/note= "This region is absent in rat autotaxin
sequence (AAY71986)"
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                                                                                                                                                                                                        Rat brain autotaxin designated as PD-Ialpha
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126..128
/label= RGD_binding_domain
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83.6%; Pred. No. 0;
:ive 33; Mismatches
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AAY71989 standard; Protein;
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                                                                                       TLPDHERPSVYAFYSEQPDFSGHKYGPFGPEESSYGSPFTPAKRPKRKVAPKRRQERPVA
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AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. The tumourous form of ATX is a secreted protein, while the transmembrane bound form is not present in tumour cells. The cDNA encoding this sequence can be used in a vector, to transform cells. The recombinant cells can then be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protein are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXT, while having little effect on the membrane form of AXT.
stimulating protein; AMF;
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Autotaxin derived from human liver cells

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an autocrine motility stimulating protein which is present in cancer cells. ATX stimulates both random and directed migration of melanoma cells. ATX stimulates both random and directed migration of melanoma transmembrane bound form of ATX is a secreted protein, while the transmembrane bound form is not present in tumour cells. The cDNA encoding this sequence can be used in a vector, to transform cells. The recombinant cells can then be used to produce the peptide sequences. Antibodies specific for these sequences can be produced, and can be used in cancer diagnosis and therapy. Different sites of localisation of the protesn are utilised for diagnosis and prognosis of the stages of tumour progression. The sequences can be used in treatment methods to advantageously block the activity of the secreted form of AXT, while having little effect on the membrane form of AXT. Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF 249 CDNLCKSYTSCCHDFDELCLKTARGWECTKDRCGEVRNEENACHCSEDCLARGDCCTNYQ 135 136 VVCKGESHWVDDDCEEIKAAECPAGFVRPPLIIFSVDGF--RASYMKKGSKVMPNIEKLR 193 WWGGQPLWITATKQGVKAGTFFWSVVI----PHERRILTILRWLTLPDHERPSVYAFYSE 309 234 QPDFSGHKYGPFGPEESSYGSPFTPAKRPKKVAPKRRQERPVAPPKKRRKIHRMDHYA 369 AETRODKMTNPLREIDKIVGOLMDGLKQLKLRRCVNVIFVGDHGMEDVTCD--RTEFLSN 427 487 nseq SCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGIVGNSMYDPVFDATFHLRGREKFNHR YLTNVDDITLVPGTLGRIRSKFSNNAKYDPKAIIANLTCKKPDQHFKPYLKQHLPKRLHY AAR86559-R86596 represent autotaxin (ATX) and fragments of it. Length 788; Autotaxin motility stimulating protein, and DNA encoding it in cancer diagnosis and therapy Σ tumour; antibody; cancer diagnosis; therapy Stracke DB 17; ыì qpdfsghkhmpfgpe------Schiffmann 12; Mismatches 76.5%; Score 3842; 85.6%; Pred. No. 0; USSH ) US DEPT HEALTH & HUMAN SERVICES Claim 4; Page 62-65; 112pp; English. Murata J, 94US-0346455 94US-0249182 Best Local Similarity 85.69 Matches 727; Conservative Liotta L, WPI; 1996-020533/02 AA; N-PSDB; AAT06613. 788 melanoma cell; W09532221-A2 25-MAY-1994; 24-MAY-1995; 28-NOV-1994; J, 30-NOV-1995 Sequence Query Match Krutzch 94 310 250 428 Homo 61 194 119 254 179 235 370 g ò g ö ŏ ŏ ò g δλ g g Óγ

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